

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 05-07-02

Searcher: Beverly C. 4919

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 2.8

Number of Searches: _____

Number of Databases: 1

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other CGN

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 16:24:41 ; Search time 117.39 seconds
(without alignments)
161.536 Million cell updates/sec

Title: US-09-534-229C-1

Perfect score: 1362

Sequence: 1 MARFAALAYCAAAALLAVAA.....MLGTATCGNLDCTQRFAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	256	22	AA11487
2	1277	93.8	252	20	AAW98081
3	1196	87.8	230	20	AAW98082
4	992	72.8	252	21	AA118903
5	846.5	62.2	253	16	AA176714
6	822.5	60.4	253	16	AA176712
7	816.5	59.9	250	16	AA176713
8	814.5	59.8	254	12	AA13274
9	814.5	59.8	254	18	AAW31296
10	814.5	59.8	254	21	AA1807512
11	798	58.6	323	22	AA11488

12	772	56.7	266	15	AARS2577	Chitinase G. Hord
13	756.5	55.5	292	18	AAW24554	Chitinase. Cucurb
14	747.5	54.9	336	13	AAAR29019	RCH10 chitinase pr
15	747.5	54.9	336	16	AAAR67969	Rice chitinase. O
16	737.5	54.1	259	21	AA118902	A maize chitinase
17	737.5	54.1	336	22	AA118904	Amino acid sequenc
18	736	54.0	298	20	AAW98080	Rye chitinase-like
19	736	54.0	318	20	AAW98079	Rye chitinase-like
20	734	53.9	319	22	AA11489	Wheat chitinase pr
21	731	53.7	317	17	AAW00186	American elm chiti
22	728	53.5	243	20	AAW90169	C. ensiformis chit
23	710.5	52.2	328	13	AAAR20822	Sequence of endoch
24	710.5	52.2	329	15	AAAR56860	Endochitinase prec
25	707.5	51.9	324	12	AA113275	Tobacco intracellu
26	707.5	51.9	324	18	AAW31297	Nicotiana sp. intr
27	707.5	51.9	324	21	AAW07513	Amino acid sequenc
28	701	51.5	329	12	AA115841	Basic chitinase 48
29	697	51.2	331	12	AA111305	Chitinase encoded
30	658	48.3	328	19	AAW64776	Floral organ-speci
31	648.5	47.6	303	13	AAAR20820	Sequence of a 302
32	629	46.2	439	13	AAAR28150	Sugar beet chitina
33	610.5	44.8	272	21	AAAG28415	Arabidopsis thalia
34	610.5	44.8	280	21	AAAG28414	Arabidopsis thalia
35	602	44.2	284	21	AA118905	A maize chitinase
36	594.5	43.6	2466	20	AAV05844	Banana ripening fr
37	474	34.8	372	22	AAAB28788	protein encoded by
38	462.5	34.0	155	21	AA118906	Amino acid sequenc
39	407.5	29.9	268	13	AAAR28147	Sugar beet chitina
40	398.5	29.3	281	21	AA118894	A maize chitinase
41	389.5	28.6	271	21	AA118904	Amino acid sequenc
42	389.5	28.6	271	21	AA118936	Sugar beet chitina
43	383.5	28.2	264	13	AAAR28145	S. lavendulae Mmcy
44	366	26.9	271	21	AA132539	Chitinase amino ac
45	337	24.7	294	21	AA135811	

ALIGNMENTS

RESULT 1

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ID  AA11487
XX  AA11487 standard; protein; 256 AA.
XX  AA11487;
XX  02-MAR-2001 (first entry)
XX  Wheat chitinase protein homologous to barley chitinase.
XX  Wheat; chitinase; low temperature expression; hardened; plant;
XX  snow mould resistance; psychophilic plant pathogen; barley.
XX  Triticum aestivum.
XX  JP20000270866-A.
XX  03-OCT-2000.
XX  25-MAR-1999; 99JP-0081694.
XX  25-MAR-1999; 99JP-0081694.
XX  (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
XX  WPI; 2001-027417/04.
XX  New low temperature expression chitinase gene for producing a plant
XX  grade highly resistant to psychophilic plant pathogenic microbes
XX  Claim 1; Fig 1; lipp; Japanese.
XX  This invention describes novel wheat chitinase genes. The invention also
XX  describes a method for the isolation of a low temperature expression
CC

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CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.

SQ Sequence 256 AA;

Query Match 100.0%; Score 1362; DB 22; Length 256;
 Best Local Similarity 100.0%; Pred. No. 8.4e-127;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARFALAVCAALLAVAGAAAGVGSVITRSVYASMLPNRNSLCPARGFTYDAF 60
 DB 1 marfaalavcaallavagaaagvgsvitrsvyasmlpnrnsldcpargfitydaf 60
 QY 61 IAAANTFPGFTGSGADDIKRDIAAFPGTSHETTGTRGAADQFGWGYCFKEEISKATS 120
 DB 61 iaantfpgftgsgaddikrdlaafgtshtettgtrgaadqfgwgycfkeeiskats 120
 QY 121 PPYGRGPQLTGRSNYDLAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSK 180
 DB 121 ppygrgpqltgrsnydlagkdlvsnpdlvstdavvsfrtamfwmtaagnkpsk 180
 QY 181 HNVALLRRWPTAADAAGRVPGYGVITNTINGLCEGMRNDANVDRIGYTRYCGMLGT 240
 DB 181 hnvalrrwptadaagrvpgygvitntinglcegmrgndanvdrigytrycgmlgt 240
 QY 241 ATGGNLDCTQNRNAS 256
 DB 241 atggnldcytqrnfas 256

RESULT 2
 AAW98081
 ID AAW98081 standard; Protein; 252 AA.

AC AAW98081;

DT 21-JUN-1999 (first entry)

DE Rye chitinase-like protein CHW46 preprotein.

KW CHW46; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.

OS Secale cereale.

FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /note= "signal peptide"
 FT 23..252
 FT /note= "mature protein, also claimed in Claim 10"

XX WO9906565-A2.

PN 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

DR N-PSDB; AAX24890.

XX New nucleic acid encoding antifreeze polypeptides from plants -

PT particularly with chitinase activity, used to impart frost, and

PT pathogen, resistant to plants, for preservation of foods, cells etc.

PT and for treating tumours

XX Claim 10; Fig 22d; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)

CC CHW46 preprotein. The mature protein, which is also claimed, is a

CC chitinase-like protein that has chitinase (antifungal) and

CC antifreeze activities. CHW46 cDNA (see AAX24890) was obtained by

CC isolating mRNA from rye plants grown at low temperatures in the

CC absence of pathogens or other stresses, i.e. under conditions when

CC only chitinases with antifreeze activity would be expressed.

CC CHW46 and CHT9 (see AAW98079-80) have been cloned and expressed in

CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.

CC The chitinase-like antifreeze proteins can be used to increase

CC freezing tolerance of plants and microorganisms; to increase field

CC survival of plants, animals and microorganisms exposed to sub-zero

CC temperatures; to inhibit ice recrystallisation in biological

CC materials or foods; for cryopreservation and hypothermic protection

CC of cells, embryos, tissues etc. (particularly human platelets); and

CC to kill tumour cells. They are also used to inhibit initiation and

CC progression of diseases or spoilage caused by low temperature

CC pathogens (particularly fungi) in plants, frozen foods and any

CC cryopreserved biological material. The signal peptide can be used

CC to direct protein secretion in transgenic organisms or expression

CC systems.

XX Sequence 252 AA;

SQ

Query Match 93.8%; Score 1277; DB 20; Length 252;
 Best Local Similarity 93.8%; Pred. No. 2.1e-118;
 Matches 240; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARFALAVCAALLAVAGAAAGVGSVITRSVYASMLPNRNSLCPARGFTYDAF 60

DB 1 marfaal-----aalllavagaaagvgsvitqsmysamlpnrnsldcpargfitydaf 56

QY 61 IAAANTFPGFTGSGADDIKRDIAAFPGTSHETTGTRGAADQFGWGYCFKEEISKATS 120

DB 57 iaantfpgftgsgaddikrdlaafgtshtettgtrgaadqfgwgycfkeeinkats 116

QY 121 PPYGRGPQLTGRSNYDLAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSK 180

DB 117 ppygrgpqltgrsnydlagkdlvsnpdlvstdavvsfrtamfwmtaagnkpsk 176

QY 181 HNVALLRRWPTAADAAGRVPGYGVITNTINGLCEGMRNDANVDRIGYTRYCGMLGT 240

DB 177 hnvalrrwptadaagrvpgygvitntinglcegmrgndanvdrigytrycgmlgt 236

QY 241 ATGGNLDCTQNRNAS 256

DB 237 atggnldcytqrnfas 252

RESULT 3

AAW98082

ID AAW98082 standard; Protein; 230 AA.

AC AAW98082;

DT 21-JUN-1999 (first entry)

DE Rye chitinase-like protein CHW46.

XX CHW46; chitinase-like protein; antifreeze protein; AFP;

XX winter rye; antifungal; fungicide; cold tolerance; frost tolerance;

XX transgenic plant; preservation; cryopreservation; tumour; therapy.

XX Secale cereale.

XX WO9906565-A2.

XX 11-FEB-1999.

PD

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XX PF 31-JUL-1998; 98WO-CA00745.
XX PR 31-JUL-1997; 97US-0903872.
XX PA (ICEB-) ICE BIOTECH INC.
XX PI Griffith M, Hew C, Moffatt B, Xiong F;
XX WPI; 1999-153795/13.
XX DR N-PSDB; AAX24890.
XX PT New nucleic acid encoding antifreeze polypeptides from plants -
XX PT particularly with chitinase activity, used to impart frost, and
XX PT pathogen, resistant to plants, for preservation of foods, cells etc.
XX PT and for treating tumours
XX PS Claim 10; Fig 22c; 118pp; English.
XX CC The present sequence is winter rye (Secale cereal L. cv. Muskateer)
XX CC CH146 mature protein. It lacks the 22-amino acid signal peptide
XX CC of the preprotein (see AAW98081), which is also claimed. Mature
XX CC CH146 is a chitinase-like protein that has chitinase (antifungal)
XX CC and antifreeze activities. CH146 preprotein cDNA (see AAX24890) was
XX CC obtained by isolating mRNA from rye plants grown at low temperatures
XX CC in the absence of pathogens or other stresses, i.e. under conditions
XX CC when only chitinases with antifreeze activity would be expressed.
XX CC CH146 and CH19 (see AAW98079-80) have been cloned and expressed in
XX CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
XX CC The chitinase-like antifreeze proteins can be used: to increase
XX CC freezing tolerance of plants and microorganisms; to increase field
XX CC survival of plants, animals and microorganisms exposed to sub-zero
XX CC temperatures; to inhibit ice recrystallisation in biological
XX CC materials or foods; for cryopreservation and hypothermic protection
XX CC of cells, embryos, tissues etc. (particularly human platelets); and
XX CC to kill tumour cells. They are also used to inhibit initiation and
XX CC progression of diseases or spoilage caused by low temperature
XX CC pathogens (particularly fungi) in plants, frozen foods and any
XX CC cryopreserved biological material.
XX SQ Sequence 230 AA;

Query Match 87.8%; Score 1196; DB 20; Length 230;
Best Local Similarity 95.6%; Pred. No. 2e-110;
Matches 219; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 28 VGSVTRSYASMLPNRNSLCPARGFTYDAFIAAANFPFGTGTGSADDIKRDLAFFF 87
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 vgsvitqmyasmLPDRNSLCPARGFTYDAFIAAANFPFGTGTGSADDIKRDLAFFF 61

QY 88 GQTSHTTGGTGAADQFGWGYCFKEEISKATSPYPYGRGPQLTGSRNYDLAAGRAIGKD 147
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 gqtshttgtrgaadqfgwgycfkeeinkatspypyrgpqltgrsnydlagraigkd 121

QY 148 LVSNPDLYSTDAVVSFRTAMFWMTAOGNKPCHNVALRRWPTTADTAAGRVPGYGVIT 207
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 lvsnpdlystdavvsfrtawfwmmtaognkpchshvalrrwtptadnaagrvpygvit 181

QY 208 NIINGGLECGMRNDANVDRIGYTRYCGMLGTATGNGNLDCTYQRNFAS 256
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 niingglecgmrndanvdrigyytrycgmlgtatgngnldctyqrnf 230

RESULT 4
AAB18903
ID AAB18903 standard; Protein; 252 AA.
XX AC AAB18903;
XX XX
DT 08-FEB-2001 (first entry)
XX DE A maize chitinase polypeptide designated zmCh15.

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XX KW Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase family 18;
XX KW pathogen control; disease resistance; molecular marker.
XX OS Zea mays.
XX PN WO200056908-A2.
XX PD 28-SEP-2000.
XX PF 09-MAR-2000; 2000WO-US06121.
XX PR 24-MAR-1999; 99US-0125915.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Simmons CR, Yalpani N;
XX DR WPI; 2000-628269/60.
XX DR N-PSDB; AAA96231.
XX PT New maize chitinase genes encoding seven chitinases of glucosyl
XX PT hydrolase family 19 are useful for enhancing disease resistance in crop
XX PT plants by modulating its expression in plants -
XX PS Claim 11; Page 85; 96pp; English.
XX CC The present sequence represents a maize chitinase polypeptide. The
XX CC specification describes glucosyl hydrolase family 19 chitinases
XX CC (AAB18994, AAB18996, AAB18999, and AAB18902-05), and glucosyl hydrolase
XX CC family 18 chitinases (AAB18995, AAB1897-98 and AAB18900-01). The level of
XX CC chitinase in plants can be modulated to enhance disease resistance in
XX CC crop plants and for control of pathogens. The chitinase polynucleotides
XX CC are also useful as molecular markers for genotype in a plant, and for
XX CC sequence shuffling.
XX SQ Sequence 252 AA;

Query Match 72.8%; Score 992; DB 21; Length 252;
Best Local Similarity 72.8%; Pred. No. 3.6e-90;
Matches 187; Conservative 23; Mismatches 39; Indels 8; Gaps 3;

QY 1 MARFA--ALAVCAAAALLAVAA3GAAAGQGVSVITRSVYASMLPNRNSLCPARGFTYTD 58
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 marfalvacaaataalil-----gvaadvasiitqdyvngmlpdrdtqcpangfytyd 55

QY 59 ATIAAANFPFGTGTGSADDI-KRDLAEPFGQTSHTTGGTGAADQFGWGYCFKEEISK 117
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 atiqavnfpgtfgtsstdelnkrelaatfgtshettggtgaadqfgwgycfkeeink 115

QY 118 AUPPPYVGRGPQLTGSRNVDLNGRAIGKDLVSNPDLYSTDAVVSFRTAMFWMTAOGN 177
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 aupsppyyrgpqltgrsnydngraigkdlsnlpdlystdavvsfktalwfwmtaogpk 175

QY 178 PSCHNVALRRWPTTADTAAGRVPGYGVITNIINGLECGMRNDANVDRIGYTRYCGM 237
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 pschdvlgnwtpssadaaagrvpygaitniingakdcgvgqnaandrigytrycdm 235

QY 238 LGTATGGNLDCTYQRNF 254
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 lgvgygdnlcdysqghf 252

RESULT 5
AAR76714
ID AAR76714 standard; Protein; 253 AA.
XX AC AAR76714;
XX XX
DT 06-DEC-1995 (first entry)
XX DE Tobacco endochitinase PR-Q precursor.

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Db 245 cyngrnfa 252

RESULT 11
AAB11488
ID AAB11488 standard; protein; 323 AA.
AC AAB11488;
XX
XX 02-MAR-2001 (first entry)
XX
XX Wheat chitinase protein homologous to rye chitinase.
XX
XX Wheat; chitinase; low temperature expression; hardened; plant;
XX snow mould resistance; psychophilic plant pathogen; rye.
XX
XX Triticum aestivum.
XX
XX JP2000270866-A.
XX
XX 03-OCT-2000.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
XX
XX WPI; 2001-027417/04.
XX
XX New low temperature expression chitinase gene for producing a plant
XX grade highly resistant to psychophilic plant pathogenic microbes -
XX Claim 4; Fig 2; 11pp; Japanese.
XX
XX This invention describes novel wheat chitinase genes. The invention also
XX describes a method for the isolation of a low temperature expression
XX chitinase gene in which the mRNA is extracted from a fully hardened
XX autumn wheat PI7438 (of high snow mould resistance). The genes are
XX useful for creating a plant grade, highly resistant to psychophilic plant
XX pathogenic microbes.
XX
XX Sequence 323 AA;

Query Match 58.8%; Score 798; DB 22; Length 323;
Best Local Similarity 59.8%; Pred. No. 8.3e-71;
Matches 149; Conservative 27; Mismatches 54; Indels 20; Gaps 3;

QY 22 GAAAQGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANTFPGFTGSADDIKR 81
Db 70 ggggggvasivrdlferfilhrndaaclargfytydaflaagaafpfgtgdldtrkr 129
QY 82 DLAAFGQTSHETGGTRGAAD-QFOWGYCFKEEISKATSP-----YY 124
Db 130 evaaffgtshtetggwptapdpfpfsgycfkqg---qgsppsycdgsadwpcapgkyy 186
QY 125 GRGPIQLTGRSNYDLAAGATGKDLVSPDLVSDAVVSFTAMFWMTAGCNKPSCHNVA 184
Db 187 grpplqlthnyngpagraigvdlinnpdlivatdptvafktafwnttdsqnkpshdvi 246
QY 185 LRRWPTAAATAAGRVPGYGVITNINGLGECGMRNDANVDRIGYVTRYCGMLGTATGG 244
Db 247 tglwtparadsaagrpgygvitnvinvgiegcmgqndkvadrigfykrycdiflglygn 306
QY 245 NLDCYTORNF 254
Db 307 nldcynqlsf 316

RESULT 12
AAR52577
ID AAR52577 standard; Protein; 266 AA.

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XX AAR52577;
XX
XX 05-DEC-1994 (first entry)
XX
XX Chitinase G.
XX
XX Antifungal; pathogen; resistance; transgenic organism; synergy;
XX crop protection; transgenic plant; chitinase; glucanase;
XX protein synthesis inhibitor; disease.
XX
XX Hordeum vulgare L.
XX
XX DB4234131-A.
XX
XX 21-APR-1994.
XX
XX 09-OCT-1992; 92DE-4234131.
XX
XX 09-OCT-1992; 92DE-4234131.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Chet I, Eckes P, Gornhardt B, Jach G, Logemann J;
XX Mundy J, Schell J, Goernhardt B;
XX
XX WPI; 1994-136599/17.
XX
XX N-PSDB; AAQ62518.
XX
XX Transgenic organisms contg. at least 2 pathogen inhibiting genes
XX - esp. plants contg. genes with antifungal activity, show
XX synergistic increase in disease resistance, also new DNA transfer
XX vectors
XX
XX Example 2; Page 13-14; 19pp; German.
XX
XX Chitinase is an enzyme which breaks down chitin, the major protein
XX in insect exoskeletons. The coding sequence may be used in the
XX construction of transgenic organisms, especially plants, to produce
XX pathogen resistant organisms. The genome of such transgenic organisms
XX preferably contains more than one gene with pathogen inhibiting
XX activity, each gene under the control of active promoters. The two
XX gene products then show a synergistic increase in pathogen induced
XX activity so that the transgenic organisms have a greater degree of
XX resistance or resistance against a wider spectrum of diseases.
XX
XX Sequence 266 AA;

Query Match 56.7%; Score 772; DB 15; Length 266;
Best Local Similarity 56.8%; Pred. No. 2.4e-68;
Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps 2;

QY 6 ALAVCAALLLAVAGAAQGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAAN 65
Db 3 slavvavvatvamaigtargssvsvraqfdmlhrndgacqakgfytydaifaavaa 62
QY 66 TFPFGFTGSADDIKRDLAAFFGQTSHETGGTRGAAD-QFOWGYCFKEEISK----- 117
Db 63 afpfgftgsadackrevaafilaqtshetggwatapdgafagwgcfcgkergassdyctp 122
QY 118 -----ATSPPYGGRGPIQLTGRSNYDLAAGATGKDLVSPDLVSDAVVSFTAMFWM 171
Db 123 saqwpccapgrkryygrgpiqlshnyngpagraigvdlilnpdlivatdvtgfktafw 182
QY 172 TAQGNKPSCHNVALRRWPTAAATAAGRVPGYGVITNINGLGECGMRNDANVDRIGY 231
Db 183 tadppkpschaviagqwspsgadragrvpfgvitnlingiegcmgqndkvadrigfy 242
QY 232 TRYCGMLGTATGGNLDCYTORNFA 255
Db 243 krycdilgvgynldcysqrpf 266

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RESULT 13
AAW24554
ID AAW24554 standard; Protein; 292 AA.
XX AC AAW24554;
XX DT 10-OCT-1997 (first entry)
XX DE Chitinase.
XX KW Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase;
KW fungal cell membrane; pathogenic fungus; disease resistance; chitin.
XX OS Cucurbita pepo.
XX PN JP09163987-A.
XX PD 24-JUN-1997.
XX PF 14-DEC-1995; 95JP-0347367.
XX PR 14-DEC-1995; 95JP-0347367.
XX PA (NIHA ) JAPAN ENERGY CORP.
XX PA (SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
XX DR WPI; 1997-380170/35.
XX DR N-PSDB; AAT79940, AAT79941.
XX KW Chitinase derived from pumpkin - used to protect plants against
PT pathogenic fungi
PS Claim 1; Page 2; 36pp; Japanese.
XX CC This sequence represents the pumpkin chitinase. Chitinase is an enzyme
CC decomposing chitin (not present in plant cell membranes) found in the
CC cell membranes of fungi. Plants have this enzyme to protect themselves
CC from pathogenic fungi. Thus this enzyme can be used to prevent plants
CC from being infected with pathogenic fungi, and the chitinase gene can be
CC introduced into plants to improve their resistance to diseases caused by
CC fungi. As the amino acid sequence of the chitinase does not have any
CC region to be cleaved by ubiquitous peptidases in cells, the chitinase
CC produced by genetic recombination technology works for various host cells
CC and serves for plant immunity to confer disease resistance on plants as
CC the host.
XX Sequence 292 AA;

Query Match 55.5%; Score 756.5; DB 18; Length 292;
Best Local Similarity 58.3%; Pred. No. 9.4e-67;
Matches 144; Conservative 26; Mismatches 64; Indels 13; Gaps 2;

QY 21 GGAAGQGVSVITRSVYASMLPNRDNLSICPARGFTTYDAFIAAATFPFGFTGTSADDIK 80
DB 46 ggggggsvsinealynqmkysxdrpcpsngfyrynaftaagdsfsgftgdaatrk 105
QY 81 RDLAAFFGQTSHETGTRGAAD-QFOWGCFKKEISK-----ATSPPYGRG 127
DB 106 relaaffgqtshettggtatpdygawgycfirengdvyscpqgwpcaagqkygrg 165
QY 128 PIQLGRSNYDLAIGKDLVSNPDVSTDAVVSFRFTAMFWMTAQGNKPSCHNVALRR 187
DB 166 pqlgthnyygpagraalnllonpdlvatpvaftaiwfmtpggnkpschdvitr 225
QY 188 WPTAADTAAGRPGVGVITNIINGLEGCMGRNANVDRIQYTRYCGMLTATYCGNLD 247
DB 226 wqpsaadsaagrpygvvitniinglegcrgdarsvadrifkrycdlligvgnnld 285
QY 248 CYTQRNF 254
DB 286 cnnqrnf 292

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RESULT 14
AAR29019
ID AAR29019 standard; Protein; 336 AA.
XX AC AAR29019;
XX DT 20-APR-1993 (first entry)
XX DE RCH10 chitinase protein.
XX KW Promoter; region; rice; chitinase; physical; biological; stress;
KW leaves; stems; roots; male; female; reporter; monocotyledon;
KW dicotyledon; development; plant; defence; selectable; genes.
XX OS Oryza sativa.
XX FH Key
XX FT Region
XX FT 123..323
XX FT Location/Qualifiers
XX FT /note= "Region conserved between class I and class
XX FT II chitinases"
XX PN W09220807-A.
XX PD 26-NOV-1992..
XX PF 21-MAY-1992; 92WO-US04282.
XX PR 22-MAY-1991; 91US-0704288.
XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX PI Lamb CJ, Zhu Q;
XX DR WPI; 1992-415785/50.
XX DR N-PSDB; AAK31407.
XX CC DNA fragment contg. chitinase gene and its regulatory region - is
CC responsive to mature plant stress and has low level expression in
CC leaves, moderate level expression in stem and high level
CC expression in roots
XX Disclosure; Page 33-34; 45pp; English.
XX CC The sequence given is encoded by the rice chitinase gene. The promoter
XX region of this gene (see AAK31407) is responsive to physical and/or
XX biological stress. The pattern of expression of this protein in mature
XX plants is characteristic. There is a low level of expression in
XX leaves, a moderate level in plant stems and the highest level in roots
XX and the male and female parts of the plant. The chitinase promoter
XX sequence may be linked to a reporter gene for expression in mono- or
XX dicotyledon plants. Expression of this reporter gene may be used to
XX study patterns of development and controlled expression of plant
XX defence genes and selectable genes.
XX Sequence 336 AA;

Query Match 54.9%; Score 747.5; DB 13; Length 336;
Best Local Similarity 57.3%; Pred. No. 8.8e-66;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGGAAAGQGVSVITRSVYASMLPNRDNLSICPARGFTTYDAFIAAATFPFGFTGTSADDI 79
DB 70 asggggsgsvaslvrsifolmllhrndaacpsnfitydafvaasaifpgfaaagadtn 129
QY 80 KRDLAAFFGQTSHETGTRGAAD-QFOWGCFKKEISK-----ATSPPY 124
DB 130 krevaafiaqtshettggwatapdgytgycfkeengagpdycqsaqwpcaagkky 189
QY 125 GRGPIQLGRSNYDLAIGKDLVSNPDVSTDAVVSFRFTAMFWMTAQGNKPSCHNVA 184
DB 125 ggggggsvsinealynqmkysxdrpcpsngfyrynaftaagdsfsgftgdaatrk 105

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Db 190 grgpiqlsynfnygpaggaigadllgdpdlvasdatvsfdtafwmtpqspkpscnava 249
QY 185 LRWPTAADTAAGRVPYGVITNIINGLECCMGNDANVDRIGYTRYCGMLGTATGG 244
Db 250 tgqwtpsaddqragrvpgygvitniingglecghgeddrigfykrycdilgvsyga 309
QY 245 NLDCTQR 252
Db 310 nldcysqr 317

RESULT 15
AAR67969
ID AAR67969 standard; Protein; 336 AA.
XX
AC AAR67969;
XX
DT 13-AUG-1995 (first entry)
XX
DE Rice chitinase.
XX
KW Chitinase; transgenic plant; disease resistance;
KW crop improvement; tobacco; Nicotiana tabacum; plant defense;
KW fungus pathogen; Cercospora nicotinae;
KW Thanatephorus cucumeris.
XX
OS Oryza sativa.
XX
FN WO9502319-A.
XX
PD 26-JAN-1995.
XX
PF 15-JUL-1994; 94WO-US07815.
XX
PR 16-JUL-1993; 93US-0093372.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Dixon RA, Lamb CJ, Maher EA, Zhu Q;
XX
WPI: 1995-067090/09.
DR N-PSDB; AAQ81346.
XX
PT Transgenic plants contg. several plant defence associated
PT proteins - have increased resistance to plant pathogens when
PT grown in crops as a food source
XX
PS Disclosure; Page 31-32; 45pp; English.
XX
CC The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and
CC an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were
CC incorporated into vectors for co-expression in transgenic tobacco,
CC resulting in improved resistance to Cercospora nicotinae and
CC Thanatephorus cucumeris fungal infection.
XX
SQ Sequence 336 AA;

Query Match 54.9%; Score 747.5; DB 16; Length 336;
Best Local Similarity 57.3%; Pred. No. 8.8e-66;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGGAAAGQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAANTFPGFTGSADDI 79
Db 70 asggggsgvasivsrslfdlmlhrndaacpasnftydafvaasafpgfaagdadtn 129
QY 80 KRDLAAFFGQTSHETGGTGAAD-QFQWGYCFKEISK-----ATSPYY 124
Db 130 krevaafiaqtshettggwatapdpytwgycfkeengagdpdycqqsagwpcagkyy 189
QY 125 GRGPIQLTGRSYDLAGRAIGKDLVSNPLVSTDAVVSPTAMWPMTAQGNKPSCNVA 184
Db 190 grgpiqlsynfnygpaggaigadllgdpdlvasdatvsfdtafwmtpqspkpscnava 249

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QY 185 LRWPTAADTAAGRVPYGVITNIINGLECCMGNDANVDRIGYTRYCGMLGTATGG 244
Db 250 tgqwtpsaddqragrvpgygvitniingglecghgeddrigfykrycdilgvsyga 309
QY 245 NLDCTQR 252
Db 310 nldcysqr 317

Search completed: May 3, 2002, 18:30:29
Job time: 7548 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:30:37 ; Search time 79.44 Seconds
(without alignments)
72,518 Million cell updates/sec

Title: US-09-534-229C-1

Perfect score: 1362

Sequence: 1 MARFAALAVCAAAALLAVAA.....MLGTATGNNLCYQTRNFAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846.5	62.2	253	1	US-08-162-475A-5
2	828.5	60.8	253	1	US-08-162-475A-2
3	816.5	59.9	250	1	US-08-162-475A-4
4	814.5	59.8	254	1	US-08-047-413-9
5	814.5	59.8	254	3	US-08-229-050-9
6	814.5	59.8	254	3	US-08-801-563-9
7	808.5	59.4	253	4	US-07-791-931-9
8	772	56.7	266	1	US-08-812-025-10
9	772	56.7	266	4	US-07-791-931-10
10	772	56.7	266	4	US-09-138-873A-10
11	747.5	54.9	336	1	US-07-704-288C-3
12	747.5	54.9	336	1	US-08-093-372-2
13	747.5	54.9	336	1	US-08-379-259-3
14	719	52.8	318	1	US-07-704-288C-9
15	719	52.8	318	1	US-08-379-259-9
16	718.5	52.8	328	4	US-07-791-931-7
17	710.5	52.2	329	2	US-08-475-427-13
18	710.5	52.2	329	2	US-07-842-165-13
19	709	52.1	328	4	US-07-791-931-5
20	707.5	51.9	324	4	US-08-047-413-11
21	707.5	51.9	324	3	US-08-229-050-11
22	707.5	51.9	324	3	US-08-801-563-11
23	705.5	51.8	254	2	US-08-475-427-1
24	705.5	51.8	254	2	US-07-842-165-1
25	705.5	51.8	254	4	US-08-448-398-3
26	705.5	51.8	310	4	US-07-791-931-6
27	703	51.6	330	1	US-07-704-288C-8

28	703	51.6	330	1	US-08-379-259-8	Sequence 8, Appli
29	696	51.1	310	1	US-07-704-288C-6	Sequence 6, Appli
30	696	51.1	310	1	US-08-379-259-6	Sequence 6, Appli
31	689.5	50.6	314	1	US-07-704-288C-7	Sequence 7, Appli
32	689.5	50.6	314	1	US-08-379-259-7	Sequence 7, Appli
33	654.5	48.1	302	2	US-08-475-427-6	Sequence 6, Appli
34	654.5	48.1	302	2	US-07-842-165-6	Sequence 6, Appli
35	566.5	41.6	316	4	US-07-791-931-8	Sequence 8, Appli
36	474	34.8	372	4	US-07-791-931-4	Sequence 37, Appl
37	438	31.4	130	3	US-08-329-799-37	Sequence 35, Appl
38	213	15.6	148	3	US-08-329-799-35	Sequence 2, Appli
39	82	6.0	3739	3	US-09-320-878-2	Sequence 33, Appl
40	82	6.0	3739	4	US-09-105-537-33	Sequence 6, Appli
41	82	6.0	11877	4	US-09-105-537-6	Sequence 100, App
42	81.5	6.0	249	4	US-09-413-814-100	Sequence 1, Appli
43	80.5	5.9	285	3	US-09-141-821-1	Sequence 6, Appli
44	79	5.8	922	4	US-08-450-269C-6	Sequence 6, Appli
45	78	5.7	1026	2	US-08-542-003-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-162-475A-5
; Sequence 5, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162.475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Nicotiana tabacum
US-08-162-475A-5

Query Match 62.2%; Score 846.5; DB 1; Length 253;
Best Local Similarity 63.9%; Pred. No. 4.5e-82;
Matches 159; Conservative 32; Mismatches 51; Indels 7; Gaps 3;
QY 6 ALAVCAALLAAVAGGAAAGVSVTRVYASMLPRNRDNLCPARGFTYDAFAAAN 65
Db 9 ALFCCVFFLELT----GSLAQGIGSVTSDLFNMELKNRNDGRCPANGFTYDAFAAAN 64


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QY 66 TFGGTGCGSADDIKRDLAFAFGGTSHTTGGTRGAADQFQWGYCFKKEISKATSPPYIG 125
Db 65 SFPFGTGGTDDTARKKEAFAFGGTSHTTGGSL-SAEFFTGGYCFVRQNDQ--SDRYIG 121
QY 126 RPTGTLGRSNVDLAGRAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPSCHNVAL 185
Db 122 RPTGLTNENYKEAFAIGQLVNNPDVATDATISFKTAIFWMTAQGNKPSCHDVII 181
QY 186 RWTPTAADTAAGRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLGTATG 245
Db 182 GRWTPSAADOANRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLNVPGEN 241
QY 246 LDCYQORNF 254
Db 242 LDCYNQORNF 250

RESULT 2
US-08-162-475A-2
; Sequence 2, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Lycopersicon chilense
US-08-162-475A-2

Query Match 60.8%; Score 828.5; DB 1; Length 253;
Best Local Similarity 61.6%; Pred. No. 3.7e-80;
Matches 157; Conservative 32; Mismatches 59; Indels 7; Gaps 3;

QY 3 REAALAVCAALLAAGAAGGAGVSVTRSVYASMLPNRDNLSLCPARGFYTYDAFIA 62
Db 2 KENTVSPVSLCSLFFLELTGLAQNAGSIVTRLEFQMLSFRRNDACPAKGFYTYDAFIA 61
QY 63 AANTFPFGTGSADDIKRDLAFAFGGTSHTTGGTRGAADQFQWGYCFKKEISKATSP 122
Db 62 AANFPFGGTGDDTARKKEAFAFGGTSHTTGGSGAGT---FTGGYCFVRQIDQ--SDR 116

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QY 123 YYGRGPIQLTGRSNVDLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPS 180
Db 117 YYGRGPIQLTGRSNVDLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPS 176
QY 181 HVALRRTPTAADTAAGRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLGT 240
Db 177 HNVIGQWTPSPADTAANRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLNV 236
QY 241 ATGNLDCYQORNF 255
Db 237 PTGENLDCNNQKFA 251

RESULT 3
US-08-162-475A-4
; Sequence 4, Application US/08162475A
; Patent No. 5656474
; GENERAL INFORMATION:
; APPLICANT: Zohreh Tabaeizadeh
; TITLE OF INVENTION: A novel endochitinase gene
; TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
; TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARY & CUSHMAN
; STREET: 1100 New York Avenue, N.W., 9th Floor
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 kb diskette
; COMPUTER: IBM PS/2, Model 30
; OPERATING SYSTEM: PC-DOS 3.30
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,475A
; FILING DATE: December 7, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, Paul E. Jr.
; REGISTRATION NUMBER: 32011
; REFERENCE/DOCKET NUMBER: PEW/3122/204351
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Lycopersicon chilense
US-08-162-475A-4

Query Match 59.9%; Score 816.5; DB 1; Length 250;
Best Local Similarity 62.3%; Pred. No. 6.8e-79;
Matches 154; Conservative 30; Mismatches 56; Indels 7; Gaps 3;

QY 11 AAALLAAGAAGGAGVSVTRSVYASMLPNRDNLSLCPARGFYTYDAFIAANTFP 70
Db 7 ALSCLFFLELTGLAQNAGSIVTRLEFQMLSFRRNDACPAKGFYTYDAFIAANSFPG 66
QY 71 GTTGSADDIKRDLAFAFGGTSHTTGGTRGAADQFQWGYCFKKEISKATSPPYGRGPIQ 130
Db 67 GTTGDDTARKKEAFAFGGTSHTTGGSGAGT---FTGGYCFVRQIDQ--SDRYIGR 121
QY 131 LTGGSNDVLAGRAI--GKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPSCHNVALRW 188
Db 122 LTHOSNTERAGGQIGVQDLVNNPDVATDPIISFKTAIFWMTAHNKPCHNVIIGQW 181
QY 189 TPTAADTAAGRVPGYGVITNIINGGLECGMRNDANVDRIGYTRYCGMLGTATGGN 248

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DB 182 TSPDANRVPYGVYTIININGLEONMGENTAVESRIGFYRRYCGMLNVPYTGENDLC 241
QY 249 YTORNFA 255
DB 242 NNCKNFA 248
RESULT 4
US-08-047-413-9
; Sequence 9, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/047,413
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; NAME: Murashige, Kate H.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-047-413-9
Query Match 59.8%; Score 814.5; DB 1; Length 254;
Best Local Similarity 62.1%; Pred. No. 1.1e-78;
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;
QY 8 AVCAALLLAVAGGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAANTF 67
DB 6 SVLALSFVFLFTGLAQNVGSIVTSLFDQMLKNRDNARCFVAVRFYTYDAFIAAANSF 65
QY 68 PFGFTGSADDIKRDLAAEFQGTSHETTGTRGAADQFQWGYCFKEISKATSPPPYGRG 127
DB 66 PFGFTGDDTARKKEIAFAFFGOTSHETTGTLSPDGPYAGGYCFLE-QNMGNGIYGRG 124

QY 128 PIQLTGRSNYDLAIGKDLVSNPOLVSTDAVVSPTAMFWMTAQGNKPSCHNVALLR 187
DB 125 PIQLTGOSNYDLAIGKDLVSNPOLVSTDAVVSPTAMFWMTAQGNKPSCHNVALLR 184
QY 188 WPTAADAAGRVPGYGVYTIININGLECGMGRDANDVDRIGYTYCYGMLGTATGGLD 247
DB 185 WTPSAADTSANRVPGYGVYTIININGLECGKGQGNARVEDRIGYTYRRNVSMNVAPGDLN 244
QY 248 CYTORNFA 255
DB 245 CYNORNFA 252
RESULT 5
US-08-229-050-9
; Sequence 9, Application US/08229050
; Patent No. 6066491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-229-050-9
Query Match 59.8%; Score 814.5; DB 3; Length 254;
Best Local Similarity 62.1%; Pred. No. 1.1e-78;
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;
QY 8 AVCAALLLAVAGGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAANTF 67

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: | : : : | | | : : | | : : | | : : : | | : : : | | : : : | | : : : |
Db 6 SWALSFVVFLLGTGLAQNVSIVISDLEFOMLKNDARCFVAFYTYDAFAANSP 65

QY 68 PFGFTGTSADDOIKRDLAAFFGQTSHETGGTGGGAADQFQWGYCFKEISKATSPPYGGR 127
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 PFGFTGDDTARKKEIAFAFFGQTSHETGGTGLSPDGPVAGGYCFLE-GNOMENGYGGR 124

QY 128 PIQLTGRSNYDLAIGRAIKGDLVNSPDLVSDAVVSTFATWFWTAOGNKPFSCHNVALR 187
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 PIQLTQSNYDLAIGRAIQDLVNNPDLVATDATVTSFKTALFNMIPGCKPSCHDVITGR 184

QY 188 WPTAADTAAGRVPGYGVYTNINGLRCGGRNDANVDRIGYTYRVCGLMGLSTATGSLD 247
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 WTPSADT5ANRVPGYGVYTNINGLRCGGRNDANVDRIGYTYRVCGLMGLSTATGSLD 244
| | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 248 CYTQRNFA 255
| | | | |

Db 245 CYNRNFA 252
| | | | |

RESULT 6
US-08-801-563-9
; Sequence 9, Application US/08801563
; Patent No. 6087560
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,563
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,413
; FILING DATE: 19-APR-1993
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-812-025-10
; Sequence 10, Application US/08812025
; Patent No. 5804184

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Transgenic pathogen-resistant organism

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812,025

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Tenser, Arthur

; REGISTRATION NUMBER: 18,839

; NAME: Kole, Lisa

; REGISTRATION NUMBER: 35,225

; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 408-2500

; TELEFAX: (212) 765-2519

; TELEX: 238555

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 266 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-812-025-10

Query Match 56.7%; Score 772; DB 1; Length 266;

Best Local Similarity 56.8%; Pred. No. 4e-74;

Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps 2;

Qy 6 ALAVCAAAALLAVAGGAAAGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAAN 65

Db 3 SLAVVAVVAIVAMAIGTARGSVSVISRAQFDRMLLRNDGACQAKGFYTYDAFVAAA 62

Qy 66 TFPFGTGSADDIKRDIAAFGQTSHTTGGTRCAAD-QFQWGYCFKKEISK----- 117

Db 63 APFGFTGSADAQKREVAFLAQTSHETTGWATAPDGAFAWGYCFKQERGASDYCTP 122

Qy 118 -----ATSPYYGRPIQLTGRSNYDLAIGKDVSNPDVSTDAVVSPTAMWFW 171

Db 123 SAQWPCAPGKRYIGRPIQLSHNYNGPAGRAIGVDLLANPDVATVGVFKTAIWFW 182

Qy 172 TAQGNKPSCHNVALRRWPTAATDAAGRPVGYVTIINGLEGCGMRNDANVDRIGY 231

Db 183 TAQPPKPSHVAIAGQWSPSGADRAAGRPVGPVITNIINGIECGHGDSDRVADRIGY 242

Qy 232 TRYCGMLGTATGNNLCYTORNFA 255

Db 243 KRYCDILGVGYGNLDCYSQRPPA 266

RESULT 9

US-07-791-931-10

; Sequence 10, Application US/07791931C

; Patent No. 6133507

; GENERAL INFORMATION:

; APPLICANT: Raikhel, Natasha V.

; TITLE OF INVENTION: Nettle Lectin cDNA

; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-07-791-931-10

Query Match 56.7%; Score 772; DB 4; Length 266;

Best Local Similarity 56.8%; Pred. No. 4e-74;

Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps 2;

Qy 6 ALAVCAAAALLAVAGGAAAGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAAN 65

Db 3 SLAVVAVVAIVAMAIGTARGSVSVISRAQFDRMLLRNDGACQAKGFYTYDAFVAAA 62

Qy 66 TFPFGTGSADDIKRDIAAFGQTSHTTGGTRCAAD-QFQWGYCFKKEISK----- 117

Db 63 APFGFTGSADAQKREVAFLAQTSHETTGWATAPDGAFAWGYCFKQERGASDYCTP 122

Qy 118 -----ATSPYYGRPIQLTGRSNYDLAIGKDVSNPDVSTDAVVSPTAMWFW 171

Db 123 SAQWPCAPGKRYIGRPIQLSHNYNGPAGRAIGVDLLANPDVATVGVFKTAIWFW 182

Qy 172 TAQGNKPSCHNVALRRWPTAATDAAGRPVGYVTIINGLEGCGMRNDANVDRIGY 231

Db 183 TAQPPKPSHVAIAGQWSPSGADRAAGRPVGPVITNIINGIECGHGDSDRVADRIGY 242

Qy 232 TRYCGMLGTATGNNLCYTORNFA 255

Db 243 KRYCDILGVGYGNLDCYSQRPPA 266

RESULT 10

US-09-138-873A-10

; Sequence 10, Application US/09138873A

; Patent No. 6271438

; GENERAL INFORMATION:

; APPLICANT: Transgenic pathogen-resistant organism

; TITLE OF INVENTION: Transgenic pathogen-resistant organism

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Baker & Botts

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/138,873A

; FILING DATE: August 24, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Tenser, Arthur

; REGISTRATION NUMBER: 18,839

; NAME: Kole, Lisa

; REGISTRATION NUMBER: 35,225

; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 408-2500

; TELEFAX: (212) 765-2519

; TELEX: 238555

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 266 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-138-873A-10

Query Match          56.7%; Score 772; DB 4; Length 266;
Best Local Similarity 56.8%; Pred. No. 4e-74;
Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps 2;

QY 6 ALAVCAALLAVAGAAAGVGVITRSVYASMLPNRDNLSCLPARGFTYTDFAFTAAAN 65
Db 3 SLAVVAVVAVTAVAGTARGSVSSVTSRAQDFMLLHNDGACQAKGFTYTDFAFAAAA 62
QY 66 TPGFGTTGSADDIKDLAAFGQTSHTTGTGTRGAAD-QFOWGYCFKKEISK----- 117
Db 63 APFGFTGSADAQKREVAFLAQTSHETTGWATAPDGAFAFGYCFKRGASSDYCIP 122
QY 118 -----ATSPYYGRGFIQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSPFTAMFWFM 171
Db 123 SAQWPCAPGKRYGRGFIQLSHNNYGPAGRAIGVLLANPDLVATDATVGEKTAIFWFM 182
QY 172 TAGGNKPSCHNVALRWTTAATDAGRVPGYGVITNIINGLECGMGRNDANVDRIQY 231
Db 183 TAOPPKPSSHAVTAGQWSPSGADRAAGRVPGYGVITNIINGGTECGHGQDSRVADRIGFY 242
QY 232 TRYCGMLGTATGNLDCYTORNFA 255
Db 243 KRYCDILGVGYNLDCYSORPFA 266

RESULT 11
US-07-704-288C-3
; Sequence 3, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; APPLICANT: MAHER, EILEEN A.
; APPLICANT: DIXON, RICHARD A.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-704-288C-3

Query Match          54.9%; Score 747.5; DB 1; Length 336;
Best Local Similarity 57.3%; Pred. No. 2.2e-71;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-138-873A-10

Query Match          54.9%; Score 747.5; DB 1; Length 336;
Best Local Similarity 57.3%; Pred. No. 2.2e-71;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGGAAAGVGVITRSVYASMLPNRDNLSCLPARGFTYTDFAFTAAANTFPGFTTGSADDI 79
Db 70 ASGGGSGVAVSVRSLSFLMLLHNRDAACPASNFYTDFAFAAASAFPGFAAGADTN 129
QY 80 KDLAAFGQTSHTTGTGTRGAAD-QFOWGYCFKKEISK-----ATSPYY 124
Db 130 KREVAFLAQTSHETTGWATAPDGYTGWYCFKENGAGPDYCOQSAQWPCAAGKKY 189
QY 125 GRGPIQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSPFTAMFWMTAGKNKPSCHNVA 184
Db 190 GRGPIQLSYNNYGPAGQAIGADLLGDPDLVASDATVSFDTAFWFWMTQSPKPSCHNVA 249
QY 185 LRWTPTADTAAGRVPGYGVITNIINGLECGMGRNDANVDRIQYTRYCGMLGTATGG 244
Db 250 TGOWTPSADQAGRVPGYGVITNIINGLECGHGDDRIADRIGFYKRYCDILGVSYGA 309
QY 245 NLDCYTQR 252
Db 310 NLDCYSQR 317

RESULT 12
US-08-093-372-2
; Sequence 2, Application US/08093372
; Patent No. 5530187
; GENERAL INFORMATION:
; APPLICANT: Lamb, Christopher J.
; APPLICANT: Zhu, Qun
; APPLICANT: Maher, Eileen A.
; APPLICANT: Dixon, Richard A.
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
; TITLE OF INVENTION: DISEASE RESISTANCE GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,372
; FILING DATE: 16-JUL-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-093-372-2

Query Match          54.9%; Score 747.5; DB 1; Length 336;
Best Local Similarity 57.3%; Pred. No. 2.2e-71;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;
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QY	20	AGGAAQGGVGSVITRSVYASMLPNRDNSTCPARGFYTYDAFIAAANTPFGFTTGSADDI	79
Db	70	ASGGGGSVASIVSRSLFDLMLLRHNDACPASNFYTYDAFVAASAFEGFAAAGDADTN	129
QY	80	KRLAAAFPGQTSHETGGTGAAD-QFQNGYCFKEBISK-----ATSPYY	124
Db	130	KREVAFLAQTSHETGGWATAPDGYTWGYCFKEENGAGGPDYQQSAQWPCAAGKYY	189
QY	125	GRGPIQLTGRSNDYDLAGRATGKDLVSNPDLVSDAVVSFTFAWFWMTAQGNKPSCHNVA	184
Db	190	GRGPIQLSYNFNGPAGQATGALLGDPDLVSDATVSDFTAFWFWTQSPFSPCNVA	249
QY	185	LRRWTPTAAATAAGRPVGYGVITNIINGGLECGMGENDANVDRIGYTYRYCGMLSTATGG	244
Db	250	TGQWTPPADQORAGRPVGYVITNIINGGLECGHGDDRIADRIGYKRYCDILGVSYGA	309
QY	245	NLDCTQR	252
Db	310	NLDCTSOR	317

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RESULT 13
US-08-379-259-3
; Sequence 3, Application US/08379259
; Patent NO. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-379-259-3

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Query Match	54.9%;	Score 747.5;	DB 1;	Length 336;
Best Local Similarity	57.3%;	Pred. No. 2.2e-71;		
Matches 142;	Conservative	28;	Mismatches 63;	Indels 15;
				Gaps 2;

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QY      20 AGGAAAGCGSVITRSVYASMLPNRDNLSCLPARGFTYTDAFIAAANTPPGFQTCSADDI 79
Db      70 ASGGSGGVASIVSRSLFDLMLHRNDRAACPAASNYYTDFAVAAASAFPFGFAAGDADTN 129
QY      80 KRDLAAFFGOTSHTTGTRGAAD-QFOMGYCFKKEISK-----ATSPPY 124
Db     130 KREVAFLACTSHETGGWATAPDGYFTWGVCYCFKEENGAGPDYCOQAQPWCAAGKKYY 189
QY     125 GRGPQLTGSRNVDLAGRAJGKLVSNPDLVSTDVAVSPTAMFWMTAQGNKPSCHNVA 184
Db     160 GRGPQLSYNFNGYPGAGQALGADLLGDPLVASDAVTSFDTAFWFMTQSPKPCNAVA 249
QY     185 LRWTPTAATAACRGPGYGVITIININGGLECCMGNRDANVRIGYTYTCGLMATGTGG 244
Db     250 TGOVTPSADDOAGRVPYGVITIININGGLECGHGDDRIADRIGFYKYICDILGSYGA 309
QY     245 NLDCTQR 252
Db     310 NLDYSQR 317

RESULT 14
US-07-704-288C-9
; Sequence 9, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704, 288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-9

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Query Match	52.8%;	Score 719;	DB 1;	Length 318;
Best Local Similarity	53.9%;	Pred. No. 2.2e-68;		
Matches 132;	Conservative	37;	Mismatches 64;	Indels 12; Gaps 2

QY	24	AAQGVGVITRSVYASMLPNRDNLSLPARGFYTYDAFTAAANTPPGFGWTGSADDIKRDL	83
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	63	APTDL SALSRSSTQOMLKHNDGACPAKGFYTYDAFTAAAKYPSFGNTGDTATRKREI	122

C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S48848
R:Byrjngelsson, T.; Collinge, D.B.; Green, B.; Gummeson, P.O.; Kragh, K.; Thordal-Christ
submitted to the EMBL Data Library, March 1994
A;Description: Purification, characterization and cDNA sequence of a basic chitinase fro
A;Reference number: S48847
A;Accession: S48848
A;Molecule type: mRNA
A;Residues: 1-252 <BRY>
A;Cross-references: EMBL:X78672; NID:g563488; PIDN:CAA55345.1; PID:g563489
C;Genetics:
A;Gene: cht2b
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-252/Product: chitinase cht2b #status predicted <Mat>
F:27-251/Domain: plant chitinase homology <PCH>

Db 65 SFPGFGTTGDDTARRKEIAAFPGQTSHETTTGGSL-SAEPPFTGGYCFVRQNDQ--SDRYYG 121
QY 126 RGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSCHNVAL 185
Db 122 RGPQLTNRNRYERAGRAIGELVNNPDLVATDATISFKTAIWFWMTQDNKPSHDVII 181
QY 186 RRTPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCYGMLGTATGNN 245
Db 182 GRWTPSAADQAANRPVPGYGVITNIINGLEGIGRNDAVEDRIGYTRYCYGMLNVPAGEN 241
QY 246 LDCYTQNRNF 254
Db 242 LDCYNQNRNF 250

RESULT 4
S20738
chitinase (EC 3.2.1.14) PR-Q - common tobacco
N:Alternate names: acidic chitinase PR-Q
C:Species: Nicotiana tabacum (common tobacco)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S20738
R:Linhorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meu
submitted to the EMBL Data Library, January 1990
A;Description: Constitutive expression of acidic and basic Chitinase in transgenic to
A;Reference number: S20737
A;Accession: S20738
A:Molecule type: mRNA
A;Residues: 1-253 <LIN>
A;Cross-references: EMBL:X51425; NID:g19772; PIDN:CAA35789.1; PID:g19773
C:Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 62.4%; Score 850.5; DB 2; Length 253;
Best Local Similarity 63.9%; Pred. No. 1.7e-66;
Matches 159; Conservative 33; Mismatches 50; Indels 7; Gaps 3;
QY 6 ALAVCAAAALLAVAAGAAAGQGVSVITRSVYASMLPNRDNSLCPARGFYTYDAFAAAN 65
Db 9 ALFCCVFFLELT---GSLAQIGSVITSDLFNEMLNKRNDRGCPANGFFTYDAFAAAN 64
QY 66 TFPFGTGSADDIKRLAALFFGQTSHETTTGGTGRGAADQFQWGYCFKEEISKATSPPYG 125
Db 65 SFPGFGTTGDDTARRKEIAAFPGQTSHETTTGGSL-SAEPPFTGGYCFVRQNDQ--SDRYYG 121
QY 126 RGPQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPSCHNVAL 185
Db 122 RGPQLTNRNRYERAGRAIGELVNNPDLVATDATISFKTAIWFWMTQDNKPSHDVII 181
QY 186 RRTPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCYGMLGTATGNN 245
Db 182 GRWTPSAADQAANRPVPGYGVITNIINGLEGIGRNDAVEDRIGYTRYCYGMLNVPAGEN 241
QY 246 LDCYTQNRNF 254
Db 242 LDCYNQNRNF 250

RESULT 5
S37342
chitinase (EC 3.2.1.14) chl7 precursor - tomato
C:Species: Lycopersicon esculentum (tomato)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S37342; S38837; S25635
R:Darnash, N.; Wagcmakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.
Plant Mol. Biol. 22, 1017-1029, 1993
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu
A;Reference number: S37341; MUID:94003061
A;Accession: S37342
A:Molecule type: mRNA
A;Residues: 1-247 <DAN>

C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S48848
R:Byrjngelsson, T.; Collinge, D.B.; Green, B.; Gummeson, P.O.; Kragh, K.; Thordal-Christ
submitted to the EMBL Data Library, March 1994
A;Description: Purification, characterization and cDNA sequence of a basic chitinase fro
A;Reference number: S48847
A;Accession: S48848
A;Molecule type: mRNA
A;Residues: 1-252 <BRY>
A;Cross-references: EMBL:X78672; NID:g563488; PIDN:CAA55345.1; PID:g563489
C;Genetics:
A;Gene: cht2b
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-22/Domain: signal sequence #status predicted <Sig>
F:23-252/Product: chitinase cht2b #status predicted <Mat>
F:27-251/Domain: plant chitinase homology <PCH>

QY 1 MARFAALVCAAAALLAVAAGAAAGQGVSVITRSVYASMLPNRDNSLCPARGFYTYDAF 60
Db 1 MARYAAL-----RALLAVAVGGAAGQGVSVITQSVYASMLPNRDNSLCPARGFYTYDAF 56
QY 61 IAAANTFPFGTGSADDIKRLAALFFGQTSHETTTGGTGRGAADQFQWGYCFKEEISKATS 120
Db 57 IAAANTFPFGTGSADDIKRLAALFFGQTSHETTTGGTGRGAADQFQWGYCFKEEISKATS 116
QY 121 PPIYGRPTQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPS 180
Db 117 PPIYGRPTQLTGRSNYDLAAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQGNKPS 176
QY 181 HNVALRRWPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCYGMLGT 240
Db 177 HDVALGRWPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCYGMLGT 236
QY 241 ATGNLDCYTQNRNFAS 256
Db 237 ATGNLDCYTQNRNFAS 252

RESULT 3
B34801
pathogenesis-related protein Q precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C;Accession: B34801
R:Payne, G.; Ahl, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A;Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins P
A;Reference number: A34801; MUID:90115914
A;Accession: B34801
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-253 <PAY>
A;Cross-references: GB:M29868; NID:g170313; PIDN:AAA34107.1; PID:g170314
C:Superfamily: plant chitinase; plant chitinase homology
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 62.7%; Score 854.5; DB 2; Length 253;
Best Local Similarity 64.3%; Pred. No. 7.7e-67;
Matches 160; Conservative 32; Mismatches 50; Indels 7; Gaps 3;
QY 6 ALAVCAAAALLAVAAGAAAGQGVSVITRSVYASMLPNRDNSLCPARGFYTYDAFAAAN 65
Db 9 ALFCCVFFLELT---GSLAQIGSVITSDLFNEMLNKRNDRGCPANGFFTYDAFAAAN 64
QY 66 TFPFGTGSADDIKRLAALFFGQTSHETTTGGTGRGAADQFQWGYCFKEEISKATSPPYG 125
Db 65 SFPGFGTTGDDTARRKEIAAFPGQTSHETTTGGSL-SAEPPFTGGYCFVRQNDQ--SDRYYG 121

A:Cross-references: EMBL:Z15139; NID:g19186; PIDN:CAA78844.1; PID:g19187
A:Accession: S38837
A:Molecule type: protein
A:Residues: 112-115;183-188;218-221 <DA2>
C:Genetics:
A:Gene: ch17
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-247/Product: chitinase ch17 #status predicted <MAT>
F:22-245/Domain: plant chitinase homology <PCH>

Query Match 62.4%; Score 850; DB 2; Length 247;
Best Local Similarity 63.5%; Pred. No. 1.8e-66;
Matches 158; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 7 LAVCAAAALLAVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANT 66
Db 1 MVLCCVFLFLT--GSFAQDVGTIVTSDLFNEMLNKRNDRCPAKGFYTYDAFIAAANS 57

QY 67 FPGFGTGSADDIKRDLAFFGQTSHTTGTGTRGAADQFQWGYCFKEEISKATSPYYGR 126
Db 58 FPGFGTGGDDTARKKETAAFFGQTSHTTGTGSLSADGPFAGGFCFVREGNQMS-GFYGR 116

QY 127 GPIQLTGRSNYDLAAGRAIGKDIYNSPDVSTDAVVSFTAMFWMTAOGNKPCHNVALR 186
Db 117 GPIQLTGSQNYDLAAGRAIGKDIYNSPDVSTDAVVSFTAMFWMTAOGNKPCHNVALR 176

QY 187 RWTPTAADTAAGRVPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLGTATGNNL 246
Db 177 QWTPSAADASANRPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLGTATGNNL 236

QY 247 DCYTORNFA 255
Db 237 DCYNQORNFA 245

RESULT 6
S51589
chitinase (EC 3.2.1.14) pcht28 precursor - Lycopersicon chilense
N:Alternate names: endochitinase pcht28
C:Species: Lycopersicon chilense
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S51589
R:Chen, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A:Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an acid
A:Reference number: S51588; MUID:95115667
A:Accession: S51589
A:Molecule type: mRNA
A:Residues: 1-253 <CHE>
A:Cross-references: EMBL:L19342; NID:g437018; PIDN:AAA64995.1; PID:g767828
C:Genetics:
A:Gene: pcht28
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-253/Product: chitinase #status predicted <MAT>
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 60.8%; Score 828.5; DB 2; Length 253;
Best Local Similarity 61.6%; Pred. No. 1.4e-64;
Matches 157; Conservative 32; Mismatches 59; Indels 7; Gaps 3;

QY 3 RFAALVCAALLAVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
Db 2 KENIVSPVALSCLFLTLTGAQNAAGSIYTRFELFQMLSFNRNDACPAKGFYTYDAFIA 61

QY 63 AANTFPGFGTGSADDIKRDLAFFGQTSHTTGTGTRGAADQFQWGYCFKEEISKATSP 122
Db 62 AANSFPGFGTGGDDTARKKETAAFFGQTSHTTGTGSGAGT---FTGGYCFYRQIDQ--SDR 116

QY 123 YYGRGPIQLTGRSNYDLAAGRAI--GKDIYNSPDVSTDAVVSFTAMFWMTAOGNKPSC 180
Db 117 YYGRGPIQLTGRSNYDLAAGRAI--GKDIYNSPDVSTDAVVSFTAMFWMTAOGNKPSC 176

QY 181 HNVALRRWTPPTAADTAAGRVPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLGT 240
Db 177 HNVIGQWTPSPADTAANRVPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLGT 236

QY 241 ATGNLDCYTORNFA 255
Db 237 PTGNLDCNNQKNEFA 251

RESULT 7
S20737
chitinase (EC 3.2.1.14) PR-P - common tobacco
N:Alternate names: acidic chitinase PR-P
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S20737
R:Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meu
submitted to the EMBL Data Library, January 1990
A:Description: Constitutive expression of acidic and basic chitinase in transgenic to
A:Reference number: S20737
A:Accession: S20737
A:Molecule type: mRNA
A:Residues: 1-253 <LIN>
A:Cross-references: EMBL:X51426; NID:g19770; PIDN:CAA35790.1; PID:g19771
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 60.0%; Score 817.5; DB 2; Length 253;
Best Local Similarity 61.4%; Pred. No. 1.2e-63;
Matches 153; Conservative 34; Mismatches 55; Indels 7; Gaps 3;

QY 7 LAVCAAAALLAVAAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANT 66
Db 10 LPCCVFFFLFLT---GSLAQGIGSVITNDLFNEMLNKRNDRCPANGFYTYDAFIAAANS 65

QY 67 FPGFGTGSADDIKRDLAFFGQTSHTTGTGTRGAADQFQWGYCFKEEISKATSPYYGR 126
Db 66 FPGFGTGSDDTARKKETAAFFGQTSHTTGTGSL-SAEPTGGYCFVRQNDQ--SDRYGR 122

QY 127 GPIQLTGRSNYDLAAGRAIGKDIYNSPDVSTDAVVSFTAMFWMTAOGNKPCHNVALR 186
Db 123 GPIQLTNNQNYEKAGNAIRQDILVNNPDVLTATISFKTAIWFMTAOGNKPCHNVALR 182

QY 187 RWTPTAADTAAGRVPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLGTATGNNL 246
Db 183 SWTPSAADASANRPGYGVITNIINGLEGCMGRDANVDRIYTRYCGMLNVPAGDNL 242

QY 247 DCYTORNFA 255
Db 243 DCYNQORNFA 251

RESULT 8
S51588
chitinase (EC 3.2.1.14) pcht1 precursor - Lycopersicon chilense (fragment)
N:Alternate names: endochitinase pcht1
C:Species: Lycopersicon chilense
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 22-Jun-1999
C:Accession: S51588
R:Chen, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A:Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an a
A:Reference number: S51588; MUID:95115667
A:Accession: S51588
A:Molecule type: mRNA
A:Residues: 1-250 <CHE>

A:Cross-references: EMBL:M97210; NID:g310936; PIDN:AAA64998.1; PID:g767827
C:Genetics:
A:Gene: pchtl
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase
F:1-21/Domain: signal sequence (fragment) #status predicted <SIG>
F:22-250/Product: chitinase #status predicted <MAT>
F:27-248/Domain: plant chitinase homology <PCH>

Query Match 59.8%; Score 816.5; DB 2; Length 250;
Best Local Similarity 62.3%; Pred. No. 1.5e-63;
Matches 154; Conservative 30; Mismatches 56; Indels 7; Gaps 3;

QY 11 AAAALLLAVAAAGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFAAANTPEGF 70
DB 7 ALSCLFFLFUTGTAQNAAGSIVTRELFOQLSFRNNDACPAKGFYTYDAFAAANSFPGF 66
QY 71 GTTGSAADIKRDLAFFGQTSHETTGTRGAADQFQWGYCFKKEISKATSPPYGRGPIQ 130
DB 67 GTTGDDTARKKEIAFAFGQTSHEITGGSAGT--FTGGYCFVRQIDQ--SDRYTGRGPIQ 121
QY 131 LTGRSNYDLARAI--GKDLVSNPDLVSTDVAVSFRTAMFWMTAQGNKPSCHNVALRRW 188
DB 122 LTHOSYERAGGIGVGDQVNNPDLVATPIISFKTAIFWMTAHNKPCHNVIIGQW 181
QY 189 TPTAADTAAGRVGPGVITNIINGLEGCGMGRNDANVDRIGYTRYCGMLGTATGCLNDC 248
DB 182 TSPADTAANRVGPGVITNIINGLEGCGMGPNTAVESRIGFYRYCGMLNVPITGENLDC 241
QY 249 YTORNFA 255
DB 242 NNOKNFA 248

RESULT 9
S20741
chitinase (EC 3.2.1.14) - garden petunia
N:Alternate names: acidic chitinase
C:Species: Petunia x hybrida (garden petunia)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S20741
R:Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meulen
submitted to the EMBL Data Library, January 1990
A:Description: Constitutive expression of acidic and basic Chitinase in transgenic tobac
A:Reference number: S20737
A:Accession: S20741
A:Molecule type: mRNA
A:Residues: 1-254 <LIN>
A:Cross-references: EMBL:X51427; NID:g20503; PIDN:CAA35791.1; PID:g20504
C:Superfamily: plant chitinase; plant chitinase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:29-252/Domain: plant chitinase homology <PCH>

Query Match 59.8%; Score 814.5; DB 2; Length 254;
Best Local Similarity 62.1%; Pred. No. 2.3e-63;
Matches 154; Conservative 31; Mismatches 62; Indels 1; Gaps 1;

QY 8 AYCAALLLAVAAAGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFAAANTF 67
DB 6 SVIALSFVVFLLTGLTQNVGSIVTSDFDQMLKRNDRARCPAVRFYTYDAFAAANSF 65
QY 68 PGFGTTGSADDIKRDLAFFGQTSHETTGTRGAADQFQWGYCFKKEISKATSPPYGRG 127
DB 66 PGFGTTGDDTARKKEIAFAFGQTSHEITGGLSPDGPYAGGYCFLE-RGNQMGNGYGRG 124
QY 128 PIQLTGRSNYDLARAIKGKDLVSNPDLVSTDVAVSFRTAMFWMTAQGNKPSCHNVALRR 187
DB 125 PIQLTGSNVDLAGKAEQQLVNNPDLVATVSKTAIFWMTFQGNKPSCHDVITGR 184
QY 188 WPTAADTAAGRVGPGVITNIINGLEGCGMGRNDANVDRIGYTRYCGMLGTATGCLNDC 247

DB 185 WTPSAADTSANRVPGYGVITNIINGLEGCGKQGNARVEDRIGYTRNNVSIMNVAPGDNLD 244
QY 248 CYTORNFA 255
DB 245 CYNORNFA 252

RESULT 10
T03017
probable chitinase (EC 3.2.1.14) class II - rice (fragment)
N:Alternate names: class II acidic chitinase; Rcht2
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03017
R:Kim, C.Y.; Gal, S.W.; Choe, M.S.; Jeong, S.Y.; Lee, S.I.; Cheong, Y.H.; Lee, S.H.;
Plant Mol. Biol. 37, 523-534, 1998
A:Title: A new class II rice chitinase, Rcht2, whose induction by fungal elicitor is
A:Reference number: Z14820; MUID:98278381
A:Accession: T03017
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-175 <KIM>
A:Cross-references: EMBL:L40338; NID:g2340042; PIDN:AA37516.1; PID:g2340043
A:Experimental source: cv. Cheongcheongbyeol
C:Function:
A:Description: catalyzes the hydrolysis of the beta-1,4-N-acetyl-D-glucosamine linkage
C:Keywords: glycosidase; hydrolase

Query Match 59.8%; Score 814; DB 2; Length 175;
Best Local Similarity 83.4%; Pred. No. 1.7e-63;
Matches 146; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 82 DLAAFFGQTSHTTGTGTRGAADQFQWGYCFKKEISKATSPPYGRGPIQLTGRSNYDIAG 141
DB 1 ELAAFFGQTSHTTGTGTRGSDQFQWGYCFKKEINKATSPPYGRGPIQLTGSNYQAAG 60
QY 142 RAIGKOLVSNPDLVSTDVAVSFRTAMFWMTAQGNKPSCHNVALRRWPTAADTAAGRV 201
DB 61 NALGLDLVGNPDLVSTDVAVSFRTAMFWMTAQGNKPSCHDVILGRWTFSAADTAAYRV 120
QY 202 GYGVITNIINGLEGCGMGRNDANVDRIGYTRYCGMLGTATGCLNDCYTORNFAS 256
DB 121 GYDGIITNIINGLEGCGVGNQDANVDRIGYTRYKRYCDMLGTGFGNLDYCNORNFAS 175

RESULT 11
A34801
pathogenesis-related protein p precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C:Accession: A34801
R:Payne, G.; Ahl, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A:Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins
A:Reference number: A34801; MUID:90115914
A:Accession: A34801
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <PAY>
A:Cross-references: GB:M29869; NID:g170311; PIDN:AAA34106.1; PID:g170312
C:Superfamily: plant chitinase; plant chitinase homology
F:30-251/Domain: plant chitinase homology <PCH>

Query Match 59.4%; Score 808.5; DB 2; Length 253;
Best Local Similarity 61.0%; Pred. No. 7.5e-63;
Matches 152; Conservative 34; Mismatches 56; Indels 7; Gaps 3;

QY 7 LAVCAALLLAVAAAGAAAGVGSVITRSVYASMLPNRDNLSLCPARGFYTYDAFAAANT 66
DB 10 LFCCVFFLELT---GSLAAGIGSIVTNDLFNEMLKRNDRGCRPANGFYTYDAFAAANS 65

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db 237 PTGENLDCNNQNF 251
RESULT 14
S40414
chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S40414
R:Nishizawa, Y.
submitted to the EMBL Data Library, November 1990
A:Reference number: S40414
A:Accession: S40414
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-340 <NIS>
A:Cross-references: EMBL:X56787; NID:g407471; PID:CRAA40107.1; PID:g407472
C:Superfamily: lectin-related plant chitinase; hevvin chitin-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevvin chitin-binding domain homology <HCB>
F:92-330/Domain: plant chitinase homology <PCH>

Query Match 58.6%; Score 797.5; DB 2; Length 340;
Best Local Similarity 50.3%; Pred. No. 9.4e-62;
Matches 162; Conservative 28; Mismatches 61; Indels 71; Gaps 5;

QY 2 ARFAALVACAAALLLA-----VAAGGA----- 23
I ||||| ||||| I |||||
Db 14 AALVALAALAAALATAARECGAQAAGARCPNCLCSRWGCGTTSDFCGDGCQSCSG 73
I ||||| ||||| |||||
QY 24 -----AAGVGSGVITRSVYASMLPNRDNLSLCPARGFYTYDAFIAAANTFPFGGT 72
: |||||: : : : : |||||: ||||| : |||

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Db 74 CGPTPTTPSPSDGVSIVPRDLFERLLLRNDGACPARGFYTYEFLAAAFPAFGG 133
QY 73 TGSADDIKRDLAAPPFGTSHETTGTRGAAD-QFQWGYCFKKEISKATSP----- 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 TGNTEKREVAALFQGTSHETTGWTAPDGPFSWGYCFKQE-----QNPPSDYQPSPE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 -----YGRGPIQLTGRSNYDLAIGRAIGKDLVSNPDLVSDAVSFRTAMFWMTAQ 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 WPCAPGRKYYGRGPIQLSFNFNYGAPRAIGVDLLSNPDLVATDATVSKTALWFWMTPO 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 GNKPSCHNVALRRWTPTAADAAGRVGPGYVITNIINGLECGMGRNDANVDRIQYTRY 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 GNKPSSSHVDITGRWAPSPADAAAGAPGYGVITNIINGLECGHGPDDRVANRIGFYQRY 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 CGMLGTATGNNLDCYTQRFAS 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 CGAFGIGTGGNLDYCNQRPENS 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
S39979
C:Species: Oryza sativa (rice)
C:Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S39979
R:Nishikawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice ch
A:Reference number: S39979; MUID:94049667
A:Accession: S39979
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <NIS>
A:Cross-references: EMBL:X56787
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:91-329/Domain: plant chitinase homology <PCH>

Query Match 58.4%; Score 795; DB 2; Length 339;
Best Local Similarity 50.8%; Pred. No. 1.5e-61;
Matches 161; Conservative 28; Mismatches 58; Indels 70; Gaps 5;

QY 6 ALAVCAAAALLA-----VAGGA----- 23
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 ALAVLAALATARAECGAQAAGARCPNCLCSRNGWCGTTSDFCGDCQCQSCGCGPT 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 24 -----AAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAFLAAANTPPGFGTGSAD 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 TPTPPSPSDGVSIVPRDLFERLLLRNDGACPARGFYTYEFLAAAFPAFGTGTE 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 DIRDLAAPPFGTSHETTGTRGAAD-QFQWGYCFKKEISKATSP----- 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 TRKREVAALFQGTSHETTGWTAPDGPFSWGYCFKQE-----QNPPSDYQPSPEWPCAP 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 ---YGRGPIQLTGRSNYDLAIGRAIGKDLVSNPDLVSDAVSFRTAMFWMTAQGNKPS 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 GRKYGRGPIQLSFNFNYGAPRAIGVDLLSNPDLVATDATVSKTALWFWMTPOGNKPS 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 CHNYALRRWTPTAADAAGRVGPGYVITNIINGLECGMGRNDANVDRIQYTRYCGMLG 239
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 SHDVTGRWAPSPADAAAGAPGYGVITNIINGLECGHGPDDRVANRIGFYQRYCGAFG 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 TATGNNLDCYTQRFAS 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 IGTGNNLDCYNQRPENS 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:33:16 ; Search time 78.59 seconds
(without alignments)
119.432 Million cell updates/sec

Title: US-09-534-229C-1

Perfect score: 1362

Sequence: 1 MARFAALAVCAALLAVAA.....MLGTATGGLDCTQRFAS 256

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	854.5	62.7	253	1	CHIQ_TOBAC
2	850	62.4	247	1	CHIB_LYCES
3	828.5	60.8	253	1	CHIA_LYCCI
4	814.5	59.8	254	1	CHIT_PETHY
5	808.5	59.4	253	1	CHIP_TOBAC
6	803.5	59.0	253	1	CHIA_LYCES
7	772	56.7	266	1	CH12_HORVU
8	768	56.4	322	1	CH12_BRANA
9	754.5	55.4	318	1	CH11_HORVU
10	751	55.1	322	1	CHIT_ARATH
11	747.5	54.9	336	1	CH12_ORYSA
12	739.5	54.3	314	1	CHIB_VITVI
13	723	53.1	320	1	CHIX_PEA
14	723	53.1	324	1	CH11_GOSHI
15	721.5	53.0	318	1	CH11_ORYSA
16	718.5	52.8	328	1	CHIT_PHAVU
17	718	52.7	321	1	CH11_THECC
18	711.5	52.2	327	1	CH15_PHAVU
19	711	52.2	302	1	CH12_GOSHI
20	709	52.1	328	1	CH12_SOLTU
21	708	52.0	334	1	CH13_TOBAC
22	705.5	51.8	324	1	CH12_TOBAC
23	705	51.8	316	1	CH12_SOLTU
24	705	51.8	318	1	CH11_SOLTU
25	701	51.5	329	1	CH11_TOBAC
26	699	51.3	318	1	CH13_SOLTU
27	699	51.3	324	1	CH12_PEA
28	692	50.8	322	1	CH1C_LYCES
29	670	49.2	246	1	CH1D_LYCES
30	663.5	48.7	340	1	CH16_POPTR
31	644.5	47.3	302	1	CH14_SOLTU
32	614	45.1	303	1	CH1A_POPTR
33	566.5	41.6	316	1	CH18_POPTR

ALIGNMENTS

RESULT	1	CHIQ_TOBAC	STANDARD;	PRT;	253 AA.
ID	CHIQ_TOBAC				
AC	P17514;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	01-DEC-1992 (Rel. 24, Last annotation update)				
DE	ACIDIC ENDOCHITINASE Q PRECURSOR (EC 3.2.1.14) (PATHOGENESIS-RELATED PROTEIN Q) (PR-Q).				
DE	Nicotiana tabacum (Common tobacco).				
OS	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.				
OX	NCBI_TaxID=4097;				
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RP	STRAIN=CV. XANTHI NC;				
RC	MEDLINE=90115914; PubMed=2296508;				
RX	Payne G., Ahl P., Moyer M., Harper A., Beck J., Meins F. Jr.,				
RA	Ryals J.;				
RT	"Isolation of complementary DNA clones encoding pathogenesis-related proteins P and Q, two acidic chitinases from tobacco.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:98-102(1990).				
[2]	SEQUENCE FROM N.A.				
RN	STRAIN=CV. SAMSUN; TISSUE=Leaf;				
RP	MEDLINE=92033079; PubMed=2131096;				
RX	Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,				
RA	Bol J.F., van Roekel J., Meulenhof J., Cornelissen B.J.C.;				
RT	"Analysis of acidic and basic chitinases from tobacco and petunia and their constitutive expression in transgenic tobacco.";				
RL	Mol. Plant Microbe Interact. 3:252-258(1990).				
CC	-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.				
CC	-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.				
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR FLUID FROM LEAVES.				
CC	-!- INDUCTION: DURING LOCAL NECROTIC RESPONSE TO THE TOBACCO MOSAIC VIRUS.				
CC	-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL HYDROLASES).				
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CC	EMBL; M29868; AAA34107.1; -				
DR	EMBL; X51425; CAA35789.1; -				
DR	PIR; B34801; B34801.				
DR	PIR; S20738; S20738.				

P11218 urtica dioi
P42820 beta vulgar
P29023 zea mays (m
P29022 zea mays (m
P27054 phaseolus v
Q06209 brassica na
P80052 dioscorea j
Q06016 arachis hyp
Q06012 arachis hyp
Q06013 arachis hyp
Q06015 arachis hyp
P15326 coix lachry

```
DR HSSP: P23951; 2BAA.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Pathogenesis-related protein; Hydrolase; Glycosidase;
KW Chitin degradation; Signal.
FT SIGNAL 1 24
FT CHAIN 25 253
FT VARIANT 54 54 Y -> F (IN STRAIN SAMSON).
SQ SEQUENCE 253 AA; 27632 MW; 0DED41DEA9CE196 CRC64;

Query Match 62.7%; Score 854.5; DB 1; Length 253;
Best Local Similarity 64.3%; Pred. No. 3.7e-64;
Matches 160; Conservative 32; Mismatches 50; Indels 7; Gaps 3;

QY 6 ALAVCAAAALLAVAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFTAAAN 65
DB 9 ALFCCVFFLELT---GSLAQAGISVITSDLFNEMLKRNDRGCRPANGFYTYDAFTAAAN 64

QY 66 TPFGEFTGSADDIKDLAFAFGQSHETGTGRGAADQFQWGYCFKEIKATSPPYVG 125
DB 65 SPPFGFTGDDTARKKEIAAFAFGQSHETGTGSL-SAEPTGGYCFVRNDQ--SDRYIG 121

QY 126 RPIQLTGRSNDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQNKPSCHNVAL 185
DB 122 RPIQLTNNRYEKAGTAIGQELVNNPDLVAIDATISFTAIWFMTQDNKPSSHDVII 181

QY 186 RWTPTAADTAAGRVPGYGVITNIINGLEGCGMRNDANDVIRIGYTRYCGMLGTATGNN 245
DB 182 GRWTPSAQAQANRVPGYGVITNIINGLEGCGIRNDAVEDRTGYYRRCYGLNLVAPGEN 241

QY 246 LDCYTORN 254
DB 242 LDCYNORNF 250

RESULT 2
CHIB_LYCES STANDARD; PRT; 247 AA.
AC Q05540;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ACIDIC 27 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CH17.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 112-115; 182-188 AND 218-221.
RC STRAIN=CV. MONEYMAKER;
RX MEDLINE=94003061; PubMed=8400122;
RA Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
RT "Molecular characterization of four chitinase cDNAs obtained from
RT Cladosporium fulvum-infected tomato.";
RL Plant Mol. Biol. 22:1017-1029(1993).
CC -1- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST
CC CHITIN CONTAINING FUNGAL PATHOGENS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- INDUCTION: BY FUNGAL INFECTION.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO
CC CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-
CC BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC
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CC -----
CC EMBL; Z15139; CAA78844.1; -.
CC PIR; S37342; S37342.
CC HSSP; P23951; 2BAA.
CC InterPro: IPR000726; Glyco_hydro_19.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
KW Pathogenesis-related protein; Hydrolase; Glycosidase;
KW Chitin degradation; Signal.
FT SIGNAL 1 16
FT CHAIN 17 247
FT SEQUENCE 247 AA; 26583 MW; C1163ED1D272A5E5 CRC64;

Query Match 62.4%; Score 850; DB 1; Length 247;
Best Local Similarity 63.5%; Pred. No. 8.5e-64;
Matches 158; Conservative 34; Mismatches 53; Indels 4; Gaps 2;

QY 7 LAVCAAAALLAVAGAAAGVGSVITRSVYASMLPNRNSLCPARGFYTYDAFTAAANT 66
DB 1 MVLCCVFFLELT---GSFAQDVGTIVTSDLFNEMLKRNDRCPAKGFTTYDAFTAAANS 57

QY 67 TPFGEFTGSADDIKDLAFAFGQSHETGTGRGAADQFQWGYCFKEIKATSPPYG 126
DB 65 SPPFGFTGDDTARKKEIAAFAFGQSHETGTGSL-SADGPFAGGYCFVREGNOMGS-GFYGR 116

QY 127 GPIQLTGRSNDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQNKPSCHNVALR 186
DB 117 GPIQLTGRSNDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMFWMTAQNKPSCHDVITG 176

QY 187 RWTPTAADTAAGRVPGYGVITNIINGLEGCGMRNDANDVIRIGYTRYCGMLGTATGNNL 246
DB 177 QWTPSAADAASANRQPGYGVITNIINGLEGCGKQGNFQVEDRIGFYRKYCTILNVAFGDNL 236

QY 247 DCYTORNFA 255
DB 237 DCYDQRNFA 245

RESULT 3
CHIA_LYCCI STANDARD; PRT; 253 AA.
ID CHIA_LYCCI
AC Q40114; Q40113;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ACIDIC ENDOCHITINASE PCHT28 PRECURSOR (EC 3.2.1.14).
OS Lycopersicon chilense (Solanum chilense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4083;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LA1930; TISSUE=Leaf;
RX MEDLINE=95115667; PubMed=7816027;
RA Chen R.D., Yu L.X., Greer A.F., Cheriti H., Tabaeizadeh Z.;
RT "Isolation of an osmotic stress- and abscisic acid-induced gene
RT encoding an acidic endochitinase from Lycopersicon chilense.";
RL Mol. Gen. Genet. 245:195-202(1994).
CC -1- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- INDUCTION: BY OSMOTIC STRESS AND ABSICISIC ACID.
```


Db 2 KFNIVSPVALSCLFLFTLTGTLAQNAGSIVITRELEQMLSPFNDDACPAKGYFYDARIA 61
Qy 63 AANTPPGFTGTSADDIKRDIAAFQGTSHETTGTRGAADQFQWGYCFKKEISKATPPP 122
Db 62 AANSPPGFTAGDGTARKKEIAAPFGQTSHTNGSGAGT--FTGGYCFVKQIEQ--SDR 116
Qy 123 YGGRPIQLTGRSNYDLAAGRAI--GKDLVSNPDLYSTDAVVSFRTAMFWNTAOGNKPSC 180
Db 117 YGGRPIQLTHQSNYERAGOGIGVGOELVNNPDVATPIISFKTAIFWMTTEQDNKPSC 176
Qy 181 HNVALLRRVPTAADAAGRVPGYGVYITNIINGLEGCGMRNDANDVDRIGYTRYCGMLGT 240
Db 177 HNVITGQWTPSPKDTAANVPYGVYITNIINGLEGCGMRNTAESRIGFYRKYCGMLNV 236
Qy 241 ATGGNLDCCYQNFNA 255
Db 237 PTGENLDCNNQNFNA 251

RESULT 7
ID CH12_HORVU STANDARD; PRT; 266 AA.
AC P23951;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 26 KDA ENDOCHITINASE.2 PRECURSOR (EC 3.2.1.14) (CHI-26).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;

[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=CV. PIGGY;
RX MEDLINE=91107649; PubMed=1899089;
RA Leah R., Tommerup H., Svendsen I., Mundy J.;
RT "Biochemical and molecular characterization of three barley seed
proteins with antifungal properties."
RL J. Biol. Chem. 266:1564-1573(1991).
[2]
PRELIMINARY SEQUENCE OF 24-77 AND 148-188.
RC TISSUE=Endosperm;
RA Leah R., Mikkelsen J.D., Mundy J., Svendsen I.;
RT "Identification of a 28,000 dalton endochitinase in barley
endosperm."
RL Carlsberg Res. Commun. 52:31-37(1987).
[3]
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RC TISSUE=Seed;
RX MEDLINE=93132784; PubMed=8421299;
RA Hart P.J., Monzingo A.F., Ready M.P., Ernst S.R., Robertus J.D.;
RT "Crystal structure of an endochitinase from Hordeum vulgare L.
seeds."
RL J. Mol. Biol. 229:189-193(1993).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO
CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-
BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
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DR EMBL; L34210; AAA56786.1; -;
DR EMBL; M62904; AAA32941.1; -;
DR PIR; A29104; A29104.
DR PIR; A38664; A38664.
DR PDB; 2BAA; 15-JAN-96.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Signal; 3D-structure.

FT SIGNAL 1 23 26 KDA ENDOCHITINASE 2.
FT CHAIN 24 266
FT DISULFID 46 108
FT DISULFID 120 128
FT DISULFID 227 259
FT VARIANT 205 205
FT CONFLICT 173 173
FT CONFLICT 205 205
FT TURN 26 28
FT TURN 31 37
FT TURN 38 42
FT TURN 45 46
FT TURN 49 51
FT HELIX 54 62
FT TURN 63 63
FT TURN 65 68
FT TURN 72 73
FT HELIX 74 90
FT TURN 91 91
FT TURN 96 97
FT TURN 99 100
FT STRAND 102 104
FT STRAND 111 111
FT TURN 130 131
FT STRAND 135 137
FT TURN 138 141
FT STRAND 142 143
FT STRAND 145 155
FT TURN 156 156
FT TURN 164 164
FT HELIX 165 168
FT TURN 170 182
FT TURN 186 187
FT HELIX 191 194
FT TURN 195 197
FT HELIX 203 206
FT TURN 207 209
FT HELIX 214 222
FT TURN 223 224
FT HELIX 233 249
FT TURN 250 250
FT TURN 260 261
SQ SEQUENCE 266 AA; 28155 MW; 0949BE88CC20B664 CRC64;

D -> S.
G -> A (IN REF. 1; AA SEQUENCE).
D -> S (IN REF. 1; AA SEQUENCE).

Query Match 56.7%; Score 772; DB 1; Length 266;
Best Local Similarity 56.8%; Pred. No. 2.8e-57;
Matches 150; Conservative 31; Mismatches 59; Indels 14; Gaps 2;

Qy 6 ALAVCAAAALLAVAGAGAAAGVSVITRVSYSMLPNRDNLSLCPARGFYTYDAFIAAAN 65
Db 3 SLAVVAVVAIVAMAIGTARGSVSVISRAQFDRLMLHRNDGACQAKGFYTYDAFVAAAA 62
Qy 66 TFPFGTTGSDADDIKRDIAAFQGTSHETTGTRGAAD-QFQWGYCFKKEISK----- 117
Db 63 AFPFGTTGSDADAQKREVAALTAQTSHTTGGWATAPDGAFAWGCFKQERGAASSDYCTP 122
Qy 118 -----ATSPPYGCGPTQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWNM 171
Db 123 SAQWPCAPFKRYGCGPTQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWNM 182
Qy 172 TAQGNKPSCHNVALRRWPTAADTAAGRVPYGVYITNIINGLEGCGMRNDANDVDRIGY 231


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DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 318 26 KDA ENDOCHITINASE 1.
FT DOMAIN 20 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 22 37 BY SIMILARITY.
FT DISULFID 31 43 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 53 57 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33402 MW; 42D62B2FE8041954 CRC64;

Query Match 55.4%; Score 754.5; DB 1; Length 318;
Best Local Similarity 48.1%; Pred. No. 9.5e-56;
Matches 153; Conservative 31; Mismatches 71; Indels 63; Gaps 4;

QY 1 MARFAALAVCAALLLAVA-----AGGAAQ----- 26
DB 1 MRAFLVFAVVAATAATWAAVACQSGQAGGATCPNCLCCSRFGWCGSTPYCGDGCQSCSGC 60
QY 27 -----GVGSITRSVYASMLPNRDNLSCLPARGFYTYDAFTAAANTPPGFG 71
DB 61 GGSGTPVTPTPSGGGVSSIVSRALFDRMLLRNDGACQAKGFYTYDAFAAASAFRGFG 120
QY 72 TTGSADDIKDLAAFGQTSHTGTGRGAAD-QFQWGYCFKKEISK----- 117
DB 121 TTGTGTRKREVAFLAQTSHETTGWATAPDGAFAWGYCFKQERGATSNYCTPSAQWPC 180
QY 118 ATSPYVGRGPQLTGRSDYLAGRKGDLVSNPDVSTDAVVSFRTAMFWMTAQGNK 177
DB 181 APKSYTGGRGPQLSHNYNGPAGRALGVLLRNPDLVADPTVSFTAMFWMTAQAPK 240
QY 178 PSCHNVALRWTPFAADTAAGRVPGYGVIRNINIGGLECGMRNDANVDRIGYTRYCGM 237
DB 241 PSSHAVITGQWSPGSDRAAGRVPGFYGVITNVNGIECGHGQDSRVADRIGFYKRYCDI 300
QY 238 LGTATGNLDCYTORNFA 255
DB 301 LGVGYGNLDCYSQRPEFA 318

RESULT 10
CHIT_ARATH STANDARD; PRT; 322 AA.
AC P19171;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN MQC3.32.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sanac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
RT "Isolation and characterization of the genes encoding basic and
acidic chitinase in Arabidopsis thaliana.";
RL Plant Physiol. 93:907-914(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 pl, TAC
and BAC clones.";
```

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RL DNA Res. 7:217-221(2000).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSES OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- TISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL IN ROOTS WITH LOWER
CC LEVELS IN LEAVES AND FLOWERING SHOOTS.
CC -!- INDUCTION: ETHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION
CC OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH INCLUDE A N-TERMINAL
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL; M38240; AAA32769.1; ALT_INIT.
CC EMBL; AF002047; BAB03157.1; -.
CC HSSP; P23951; 2BAA.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; Chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINBINDNG.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT SIGNAL 1 20
FT CHAIN 21 315 BASIC ENDOCHITINASE.
FT PROPEP 316 322 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 21 63 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 322 AA; 34609 MW; C9AFFE4C544FCCD7 CRC64;
```

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Query Match 55.1%; Score 751; DB 1; Length 322;
Best Local Similarity 56.8%; Pred. No. 1.9e-55;
Matches 138; Conservative 35; Mismatches 56; Indels 14; Gaps 2;

QY 28 VGSVITRSVYASMLPNRDNLSCLPARGFYTYDAFTAAANTPPGFTGSGADDIKDLAAFF 87
DB 73 LSGIISQFDDMLKRNDAACPARGFYTYDAFTAAKSPFGFTGDTATRKKEVAFF 132
QY 88 GQTSHTTGGTGAAD-QFQWGYCFKKEISK-----ATSPYVGRGPQLTG 133
DB 133 GQTSHTTGGWATAPDGPYSGWGYCFKQEQNPASDYCEPSATWPCASGKRYGPGMOLSW 192
QY 134 RSNYDLAIGKDLVSNPDVSTDAVVSFRTAMFWMTAQGNKPSCHNVALRWTPFAA 193
DB 193 NNYNGICGRAIGVDLLNPNLDVANDAVIAFAKAIWFWMTAQGNKPSCHNVALRWTPFAA 252
QY 194 DTAAGRVPGYGVITNINIGGLECGMRNDANVDRIGYTRYCGMLGTATGGLDGYTORN 253
DB 253 DRAAGRLPGYGVITNINIGGLECGMRNDANVDRIGYTRYCGMLGTATGGLDGYTORN 312
QY 254 FAS 256
DB 313 FVN 315
```

Db 250 TQWTPSADQORAGRPVGYVTIINNGLECGHEDDRIADIGFYKRYCDILGVSIGA 309

QY 245 NLDQYTOR 252
| | | | | : | |
Db 310 NLDQYSQR 317

RESULT 12
CHIB_VITVI STANDARD; PRT; 314 AA.
ID CHIB_VITVI
AC P51613;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHIT1B.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PINOT;
RX MEDLINE=98052138; PubMed=9390436;
RA Busam G., Kassemeyer H.H., Matern U.;
RT "Differential expression of chitinases in Vitis vinifera L.
RT responding to systemic acquired resistance activators or fungal
RT challenge.";
RL Plant Physiol. 115:1029-1038(1997).
CC -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

CC EMBL; 254234; CAA90970.1; -.
CC HSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBd1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 314 BASIC ENDOCHITINASE.
FT DOMAIN 21 61 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 55 59 BY SIMILARITY.
SQ SEQUENCE 314 AA; 33429 MW; 3802484ED69BC6C0 CRC64;

Query Match 54.3%; Score 739.5; DB 1; Length 314;
Best Local Similarity 48.2%; Pred. No. 1.7e-54;

RESULT 11
ID CH12_ORYSA STANDARD; PRT; 336 AA.
AC P25765;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).
GN RCH10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91238706; PubMed=2034221;
RA Zhu Q., Lamb C.J.;
RT "Isolation and characterization of a rice gene encoding a basic
RT chitinase.";
RL Mol. Gen. Genet. 226:289-296(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC PIR; S15997; S15997.
DR HSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBd1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 336 BASIC ENDOCHITINASE 2.
FT DOMAIN 22 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 24 39 BY SIMILARITY.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 336 AA; 35565 MW; 7F4EC126265DEA84 CRC64;

Query Match 54.9%; Score 747.5; DB 1; Length 336;
Best Local Similarity 57.3%; Pred. No. 3.8e-55;
Matches 142; Conservative 28; Mismatches 63; Indels 15; Gaps 2;

QY 20 AGSAAAGGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAANTFPGFTGSGADDI 79
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 70 ASGGGGGVASIVSRSLFDMLLRNDACPASNFYTYDAFAAASAFPGFAAGDADTN 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 80 KRLAAFFGQTSHTTGGTGAAD-QFQWGYCEKEELSK-----ATSPPY 124
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 130 KREVAAPLACTSHETTTGGWATDPGTYTWGCFKEENGAGPDYCOQSAOWPCAGKKY 189
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 125 GRGPIQLTGRSNYDLAGRAIGKDLVSNPDLYSTDAVYSFRTAMFWMTAGCNKPSCHNVA 184
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
Db 190 GRGPIQLSYENYCPAGCAIGADLLGPDILVASDATYSFDTAFWFWTPQSPKPSCHNA 249
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
QY 185 LRRWTPTAADTAAGRPVGYVTIINNGLECGMRNDANVDRIGYTRYCGMGTATGG 244
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |

Matches 148; Conservative 30; Mismatches 76; Indels 51; Gaps 4;

QY 1 MARFAALAVCAAAALLIA-----VAAGGAAQ----- 26

Db 1 MGLWALVAFCLLSLILVSAEGGAGGVRCPGGACCKFGWCGWNTADYCGSGCOSQCS 60

QY 27 --GVSVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANTFFGFGTGSADDDIKRLD 83

Db 61 STGDIQGLTRSMENDMLKRENGSCPGKGFYTYDAFIAAARAFPGFGTGTITTKREI 120

QY 84 AAFPGTSHETTGTRGAAD-QFQWGYCKEELSK-----ATSPPYGRGPI 129

Db 121 AALFAGTSHETTGWASAPDGPYAWGYCYLREGSGPAGYCPVSAOWPACAGRKYRGPI 180

QY 130 QLTGRNYDLAIGRAIKDLYSNPDLYSTDAVVSFRFAMFWMTAOGNKPSCHNVALRRWT 189

Db 181 QISYNYGQAGRAIGVLDVNNPDLYSTDAVVSFRFAMFWMTAOGNKPSCHNVALRRWT 240

QY 190 PTAADTAAGRPVGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGTATCGNLDY 249

Db 241 PSAGDRSAGRLPFGVYTNININGVECGKGVVQVQDRIGFYKRYCDILRVSYGNLDCN 300

QY 250 TORNEAS 256

Db 301 NORPFGS 307

RESULT 13

CHIX_PEA STANDARD; PRT; 320 AA.

AC P36907;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI_TaxID=3888;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, BIRTE; TISSUE=Leaf;

RA Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,

RA Collinge D.B.; of defence-related transcripts and cloning of a

RT "Accumulation of defence-related transcripts and cloning of a

RT chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with

RL Ascochyta blight Lib.;"

RL Plant Sci. 92:69-79(1993).

CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN

CC CONTAINING FUNGAL PATHOGENS.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF

CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -!- INDUCTION: BY FUNGAL INFECTION.

CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO

CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL

CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL

CC HYDROLASES).

CC

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CC or send an email to license@sib-sib.ch).

CC

CC EMBL: X63899; CAA45359.1; -.

DR HSSP: P02877; 1HEV

DR InterPro: IPR001002; Chitin_bind.

DR InterPro: IPR000726; Glyco_hydro_19.

DR Pfam: PF00187; chitin_binding_1.

DR Pfam: PF00182; Glyco_hydro_19; 1.

PRINTS; PR00451; CHITINBINDING.

DR ProDom; PD000574; Glyco_hydro_19; 1.

DR ProDom; PD000609; Chitin_bind; 1.

DR SMART; SM00270; ChitBD1; 1.

DR PROSITE; PS00026; CHITIN_BINDING; 1.

DR PROSITE; PS00773; CHITINASE_19_1; 1.

DR PROSITE; PS00774; CHITINASE_19_2; 1.

KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;

KW Multigene family.

FT SIGNAL 1 23 BY SIMILARITY.

FT CHAIN 24 320 ENDOCHITINASE.

FT DOMAIN 24 64 CHITIN-BINDING (BY SIMILARITY).

FT DISULFID 26 41 BY SIMILARITY.

FT DISULFID 35 47 BY SIMILARITY.

FT DISULFID 40 54 BY SIMILARITY.

FT DISULFID 58 62 BY SIMILARITY.

FT SEQUENCE 320 AA; 34507 MW; 7EDBC81AECC3435 CRC64;

Query Match 53.1%; Score 723; DB 1; Length 320;

Best Local Similarity 55.6%; Pred. NO. 4e-53;

Matches 139; Conservative 33; Mismatches 62; Indels 16; Gaps 3;

QY 19 AAGSAAQGVGVITRSVYASMLPNRNSLCPARGFYTYDAFIAAANTFFGFGTGSADD 78

Db 74 STGGG---DVGLVPSLFDQMLKYRNDGRCAGHGFGFYTYDAFIAAARSFNGFGTGGDNT 130

QY 79 IKDLAAFFGQTSHTTGTGGAAD-QFQWGYCKEELSK-----ATSPPYG 125

Db 131 KKKELAAFLAQTSHETTGWPTAPDGPYAWGYCFVSPQNTQEVYCSKDPKAPGKKYGG 190

QY 126 RGPIQLTGRSNYDLAIGRAIKDLYSNPDLYSTDAVVSFRFAMFWMTAOGNKPSCHNVAL 185

Db 191 RGPIQLTGRSNYDLAIGRAIKDLYSNPDLYSTDAVVSFRFAMFWMTAOGNKPSCHNVAL 250

QY 186 RRWPTAADTAAGRPVGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGTATGAGN 245

Db 251 GRWTPSADSSAGRPVGYGVITNIINGLEGCGMRNDANVDRIGYTRYCGMLGTATGAGN 310

QY 246 LDCYTORNFA 255

Db 311 LDCNNQSRFA 320

RESULT 14

CHIL_GOSHI STANDARD; PRT; 324 AA.

ID CHIL_GOSHI

AC Q39799;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).

OS Gossypium hirsutum (Upland cotton).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Malvales; Malvaceae; Gossypium.

OX NCBI_TaxID=3635;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV, COKER 201;

RA Leverson J.P., Chlan C.A.;

RT "Isolation of a genomic DNA clone from Gossypium hirsutum with high

RT similarity to class I endochitinase plant sequences.;"

RL (In) Plant Gene Register PGR96-054.

CC -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.

CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF

CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO

CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL

CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL

CC HYDROLASES).

CC

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CC -----
 CC EMBL: U60197; AAB67842.1; -
 CC HSP; P02877; IHEV.
 CC InterPro; IPR001002; Chitin_bind.
 CC InterPro; IPR000726; Glyco_hydro_19.
 CC Pfam; PF00187; chitin_binding; 1.
 CC Pfam; PF00182; Glyco_hydro_19; 1.
 CC PRINTS; PR00451; CHITINBINDNG.
 CC PRODOM; PD000574; Glyco_hydro_19; 1.
 CC PRODOM; PD000609; Chitin_bind; 1.
 CC SMART; SM00270; ChtBD1; 1.
 CC PROSITE; PS00026; CHITIN_BINDING; 1.
 CC PROSITE; PS00773; CHITINASE_19; 1.
 CC PROSITE; PS00774; CHITINASE_19.2; 1.
 CC KX Hydroxylase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
 CC Multigene family.
 CC SIGNAL 1 22 BY SIMILARITY.
 CC CHAIN 23 317 ENDOCHITINASE 1.
 CC PROPEP 318 324 REMOVED IN MATURE FORM (BY SIMILARITY).
 CC DOMAIN 25 64 CHITIN-BINDING (BY SIMILARITY).
 CC DISULFID 25 40 BY SIMILARITY.
 CC DISULFID 34 46 BY SIMILARITY.
 CC DISULFID 39 53 BY SIMILARITY.
 CC DISULFID 58 62 BY SIMILARITY.
 CC SEQUENCE 324 AA; 34666 MW; 9923B123EF5C7E3E CRC64;

Query Match 53.1%; Score 723; DB 1; Length 324;
 Best Local Similarity 53.3%; Pred. No. 4e-53;
 Matches 136; Conservative 35; Mismatches 66; Indels 18; Gaps 3;

QY 20 AGGAAAGVG---SVITRSVYASMLPNRNSLCPARGFTYDAFTAAANTPPGFTGSA 76
 DB 63 SGGSPAPGPGGLTSLRSTFQMLHNRNDGACPARGEFTYDAFTAAARSEFAFTGSDQ 122
 QY 77 DDIKDLAFAFGQTSHETGTGTRGADQ--FQWGYCFKEEISKATN-----P 121
 DB 123 APRKKEIAFAAFTQSHETGTGGAAGAAADPGYAWGYCYNRELAPPSSYCASDPNYCPAPGK 182
 QY 122 PYGRGPQLTGRSNLDLAGRAIGKIDVSNPDVSTDAVSPRTAMFWMTAQGNKPSCH 181
 DB 183 QYFGPGQLSNWNYNGQCGRAIGVDLLNPNPDLSDDPTISFSAFWMTQSPKPSCH 242
 QY 182 NVALLRWTPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCGMLGTA 241
 DB 243 NVIIIGAWSPSSDRAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCYDILGVS 302

QY 242 TGGNLDCTQRFN 256
 DB 303 YGNLDCYNQSPFGN 317

RESULT 15
 CHIT_ORYSA

ID CHIT_ORYSA STANDARD; PRT; 318 AA.
 AC P24626;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV. JAPONICA; TISSUE-Seedling;
 RX MEDLINE=91370895; PubMed=1893114;
 RA Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
 RA Muthukrishnan S., Reeck G.R.;
 RT "Nucleotide sequence of a rice genomic clone that encodes a class I
 endochitinase.";
 RL Plant Mol. Biol. 16:479-480(1991).
 CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
 CC CONTAINING FUNGAL PATHOGENS.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
 CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
 CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
 CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
 CC HYDROLASES).
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: X54367; CAA38249.1; -
 CC PIR; S14948; S14948.
 CC HSP; P02877; IHEV.
 CC InterPro; IPR001002; Chitin_bind.
 CC InterPro; IPR000726; Glyco_hydro_19.
 CC Pfam; PF00187; chitin_binding; 1.
 CC Pfam; PF00182; Glyco_hydro_19; 1.
 CC PRINTS; PR00451; CHITINBINDNG.
 CC PRODOM; PD000574; Glyco_hydro_19; 1.
 CC PRODOM; PD000609; Chitin_bind; 1.
 CC SMART; SM00270; ChtBD1; 1.
 CC PROSITE; PS00026; CHITIN_BINDING; 1.
 CC PROSITE; PS00773; CHITINASE_19; 1.
 CC PROSITE; PS00774; CHITINASE_19.2; 1.
 CC KW Hydroxylase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
 CC Multigene family.
 CC SIGNAL 1 18 POTENTIAL.
 CC CHAIN 19 318 BASIC ENDOCHITINASE 1.
 CC DOMAIN 19 61 CHITIN-BINDING (BY SIMILARITY).
 CC DISULFID 21 36 BY SIMILARITY.
 CC DISULFID 30 42 BY SIMILARITY.
 CC DISULFID 35 49 BY SIMILARITY.
 CC DISULFID 53 57 BY SIMILARITY.
 CC SEQUENCE 318 AA; 33695 MW; 8FD37913450CC7EB CRC64;

Query Match 53.0%; Score 721.5; DB 1; Length 318;
 Best Local Similarity 56.2%; Pred. No. 5.2e-53;
 Matches 141; Conservative 31; Mismatches 60; Indels 19; Gaps 5;

QY 19 AAGGAAAGVGSVITRSVYASMLPNRNSLCPARGFTYDAFTAAANTPPGFTGSA 78
 DB 69 SGGGS--GVASTISFLDQMLHNRNDQACRAKGYTYDAFVAANAYPDEATTADT 126
 QY 79 IKRDLAFAFGQTSHETGTGTRGAD--QFQWGYCFKEEISK-----ATSPPY 123
 DB 127 CKREVAFLAQTSHETGTGTPADPGYSGYCFKEENNGNAPTYCEPKPWCARAKY 186
 QY 124 YGRGPQLTGRSNYDLAIGRAIGKIDVSNPDVSTDAVSPRTAMFWMTAQGNKPSCHNV 183
 DB 187 YGRGPQITINYNYG-RGAGISDLNNDLVDASDA-VSEKTAFAFWMTQSPKPSCHAV 244
 QY 184 ALRRWTPTAADTAAGRVPGYGVITNIINGLEGCMGRNDANVDRIGYTRYCGMLGTA 243
 DB 245 ITCQWTPSADDAAGRVPGYGVITNIINGVEGCGHADDKVADRIGYTRYCYDILGVS 304
 QY 244 GNLDCYQRFN 254
 DB 305 DNLDCYNQRPY 315

us-09-534-229c-1.rsp

Tue May 7 10:52:13 2002

Search completed: May 3, 2002, 18:48:31
Job time: 915 sec

OM protein - protein search, using sw model

Run on: May 3, 2002, 18:32:16 ; Search time 157.87 Seconds
(without alignments)
237.193 Million cell updates/sec

Title: US-09-534-229C-1
 perfect score: 1362
 sequence: 1 MDPFAAYAVCAANLIIAVAA.....MLGTATGGNLDICYTORNFAS 256

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

SPTRMBL17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organalle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_virtebrate.*
14: sp_unclassified.*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1334	97.9	256	10	Q43764 hordeum vul
2	1277	93.8	252	10	Q9axr8 secale cere
3	1266	93.0	252	10	Q43765 hordeum vul
4	1139.5	83.7	261	10	Q9fwe9 oryza sativ
5	1128.5	82.9	261	10	O80423 oryza sativ
6	1128	82.8	249	10	Q9leht hordeum vul
7	1000	73.4	296	10	Q9fwe7 oryza sativ
8	973.5	71.5	289	10	O04271 oryza sativ
9	825.5	60.6	236	10	Q43835 solanum tub
10	822.5	60.4	251	10	Q9sBJ9 solanum tub
11	822.5	60.4	252	10	Q43834 solanum tub
12	819.5	60.2	240	10	O22568 solanum tub
13	814	59.8	175	10	O24007 oryza sativ
14	808.5	59.4	253	10	O82552 capsicum an
15	805.5	59.1	264	10	Q42515 arachis hyp
16	797.5	58.6	340	10	Q43294 oryza sativ
17	772.5	56.7	332	10	Q42839 hordeum vul
18	768	56.4	266	10	Q9fiv0 secale cere
19	767	56.3	335	10	Q9sXJ1 arabis gemm

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Query Match          97.9%; Score 1334; DB 10; Length 256;
Best Local Similarity 98.4%; Pred. No. 6.3e-107;
Matches 252; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MARFAALAVCAALLNAVAGAAACGVSIVTSRYASMLPNRDNSLCPARGFYTWDAF 60
|||||
```

1 MAREFAALVCAAAALLVAAGGAAAGVGSVITRSVYASMLPNRNSLCPARGFTYDAF 60

Q42839 hordeum vul
Q9frv0 secale cere
Q9sx41 arabis demm

7	332	10	Q42839
4	266	10	Q9FRV0

772. 76

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Db 1 MARPAALAVCAAAALLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
QY 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 120
Db 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 120
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 180
QY 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 240
Db 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 240
QY 241 ATGGNLCYTORNFAS 256
Db 241 ATGGNLCYTORNFAS 256

RESULT 2
QYAXR8
ID Q9AXR8 PRELIMINARY; PRT; 252 AA.
AC Q9AXR8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 24.8 KDa CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]

SEQUENCE FROM N.A.
Query Match 93.8%; Score 1277; DB 10; Length 252;
Best Local Similarity 93.8%; Pred. No. 4.9e-102;
Matches 240; Conservative 7; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARPAALAVCAAAALLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARPAALAVCAAAALLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 120
Db 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 176
QY 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 240
Db 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 236
QY 241 ATGGNLCYTORNFAS 256
Db 241 ATGGNLCYTORNFAS 252

RESULT 3
QYAXR8
ID Q9AXR8 PRELIMINARY; PRT; 252 AA.
AC Q9AXR8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 24.8 KDa CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]

SEQUENCE FROM N.A.
Query Match 93.0%; Score 1266; DB 10; Length 252;
Best Local Similarity 93.0%; Pred. No. 4.3e-101;
Matches 238; Conservative 9; Mismatches 5; Indels 4; Gaps 1;

QY 1 MARPAALAVCAAAALLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 60
Db 1 MARPAALAVCAAAALLAVAGCAAAQGVSVITRSVYASMLPNRDNLSLCPARGFYTYDAF 56
QY 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 120
Db 61 IAAANTFFGTTGSADDIKRDLAFFGQTSHETGTRGAADQFQWGYCFKEEISKATS 116
QY 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 180
Db 121 PYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFTAMFWMTAOGNKPSC 176
QY 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 240
Db 181 HNVALLRWTPTAADTAAGRVPGYGVITNIINGLCEGCGMRNDANVDRIYGYTRYCGMLGT 236
QY 241 ATGGNLCYTORNFAS 256
Db 241 ATGGNLCYTORNFAS 252

RESULT 4
QYAXR8
ID Q9AXR8 PRELIMINARY; PRT; 261 AA.
AC Q9AXR8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Felblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.,
RT "Oryza sativa chromosome 10 BAC OSUNB001511 genomic sequence.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC051633; AAG13608.1; -.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
SQ SEQUENCE 261 AA; 27551 MW; 773133E7813DFDBE CRC64;

Query Match 83.7%; Score 1139.5; DB 10; Length 261;
Best Local Similarity 82.7%; Pred. No. 3.2e-90;
Matches 211; Conservative 20; Mismatches 23; Indels 1; Gaps 1;

QY 3 RFALAVCAAAALLLAAVAGGAAAGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
DB 7 RFVQLAACAAASLLAAVAGGAAAGVSVITQAVFNSMLPNRNSQCPARGFYTYDAFIA 66

QY 63 AANTFPFGGTT-GSADDIKRDLAAPFGGTSHTTGGTRGAADQFOWGYCFKEEISKATSP 121
DB 67 AANSFPAGTSGGSAELIRRELAAPFGGTSHTTGGTRGSSDQFOWGYCFKEEINKATSP 126

QY 122 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWMTAQGNKPSCH 181
DB 127 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWMTAQGNKPSCH 186

QY 182 NVALLRWTPPTAATTAAGRVPGYGVITNIINGLEGCGMRNDANDVDRIGYTRYCGMLGTA 241
DB 187 DVLGRWTPSAADTAAGRVPGYGVITNIINGLEGCGMRNDANDVDRIGYTRYCGMLGAG 246

QY 242 TGGNLDCTYQNFAS 256
DB 247 YGSNLDCTYQNFAS 261

RESULT 5
ID O80423 PRELIMINARY; PRT; 261 AA.
AC O80423;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE.
GN CHIAO OR RCHT2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh Y., Yamamoto K., Sasaki T.;
RT "Nucleotide sequence of rice acidic class II chitinase Oschia2a.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016497; BAA31997.1; -.
DR HSSP; P23951; 2BAA.
DR Mendel; 31086; Oryza; Chiao0:31086.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
FT CHAIN 30 261 CHITINASE IIA.
SQ SEQUENCE 261 AA; 27601 MW; 6760C2578121E0BF CRC64;

Query Match 82.9%; Score 1128.5; DB 10; Length 261;

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Best Local Similarity 82.0%; Pred. No. 2.9e-89;
Matches 209; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

QY 3 RFALAVCAAAALLLAAVAGGAAAGVSVITRSVYASMLPNRNSLCPARGFYTYDAFIA 62
DB 7 RFVQLAACAAASLLAAVAGGAAAGVSVITQAVFNSMLPNRNSQCPARGFYTYDAFIA 66

QY 63 AANTFPFGGTT-GSADDIKRDLAAPFGGTSHTTGGTRGAADQFOWGYCFKEEISKATSP 121
DB 67 AANSFPAGTSGGSAELIRRELAAPFGGTSHTTGGTRGSSDQFOWGYCFKEEINKATSP 126

QY 122 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWMTAQGNKPSCH 181
DB 127 PYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYSTDAVVSFRTAMFWMTAQGNKPSCH 186

QY 182 NVALLRWTPPTAATTAAGRVPGYGVITNIINGLEGCGMRNDANDVDRIGYTRYCGMLGTA 241
DB 187 DVLGRWTPSAADTAAGRVPGYGVITNIINGLEGCGMRNDANDVDRIGYTRYCGMLGAG 246

QY 242 TGGNLDCTYQNFAS 256
DB 247 YGSNLDCTYQNFAS 261

RESULT 6
ID Q9LEH7 PRELIMINARY; PRT; 249 AA.
AC Q9LEH7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE II.
GN CHT2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIDAS;
RA Green R.M., Bevan M.;
RT "Isolation and characterisation of genes induced in barley during
RT powdery mildew infection.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIDAS;
RA Green R.M.;
RL Thesis (1991), University of Cambridge, UK.
DR EMBL; AJ276226; CAB99486.1; -.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19.1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
SQ SEQUENCE 249 AA; 27127 MW; ED85AB6E9E6FEB88 CRC64;

Query Match 82.8%; Score 1128; DB 10; Length 249;
Best Local Similarity 93.6%; Pred. No. 3e-89;
Matches 206; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 37 YASMLPNRNSLCPARGFYTYDAFIAAANTFPFGGTTGSADDIKRDLAAPFGGTSHTTGT 96
DB 30 YASMLPNRNSQCPGQGFYTYVREIAAANTFPFGGTTGSADDIKRDLAAPFGGTSHTTGT 89

QY 97 GTRGAADQFOWGYCFKEEISKATSPYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYS 156
DB 90 GTRGAADQFOWGYCFKEEINKATSPYYGRGPQLTGRSNYDLAAGRAIGKDLVSNPDLYS 149

QY 157 TDVVSFRTAMFWMTAQGNKPSCHNVALRWTPPTAADTAAGRVPGYGVITNIINGLEG 216

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Db 150 TDVVVFRTAIFWMTAGNKPSSHDVALGRTPTAATDAGRVPGYGVITNIIINGGLEC 209
 QY 217 GMRGRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 256
 Db 210 GMRGRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 249

RESULT 7
 Q9FWF7 PRELIMINARY; PRT; 296 AA.
 AC Q9FWF7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PUTATIVE CHITINASE.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
 RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RA "Oryza sativa chromosome 10 BAC OSUNB0015111 genomic sequence."
 RL Submitted (OC1-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC051633; AAG13590.1; -
 DR InterPro; IPR000726; Glyco_hydro.19.
 DR Pfam; PF00182; Glyco_hydro.19; 2.
 DR ProDom; PD000574; Glyco_hydro.19; 1.
 DR PROSITE; PS00773; CHITINASE_19.1; 1.
 SQ SEQUENCE 296 AA; 32169 MW; 1C0F8158ESCf119B CRC64;

Query Match 73.4%; Score 1000; DB 10; Length 296;
 Best Local Similarity 67.7%; Pred. No. 3.6e-78;
 Matches 195; Conservative 22; Mismatches 33; Indels 38; Gaps 3;

QY 3 RFALAVCAALLLAVAGAAAGGVSVITRSVYASMLPNRNSLCPARGFYTDAFIA 62
 Db 10 RFVQLAACAVAVILLAAAGAAAGGVSVITEAVFNSMLPNRNSLCPARGFYTDAFIA 69
 QY 63 AANTFPGGTT-GSADIKRDLAFAFFGQTSHETGGTGRGAADQFQWGYCFKEEISKATSP 121
 Db 70 AANSFPAGTSGGSAELIRRELAFFGQTSHETTDGTRGSSDQFQWGYCFKEEINKATSP 129
 QY 122 PYGGRPIQLTG-----RSNYDLAAGRAIGKDL 148
 Db 130 PYGGRPIQLTGFTIINTYMLNFATSLAVYPIYSINYESHAIELPSSQERAGAPGR-- 187
 QY 149 VSNPDVSTDAVSRFRTAMFWMTAAGNKKPSCHNVALRRWPTAATDAGRVPGYGVITN 208
 Db 188 --RDLVSTNAVSEFKTAIFWMTGQYKNKPSHDVILGRWTPSAADTAAAGRVPGYGVITN 245
 QY 209 IINGLEGCMGRDANVDRIGYTRCYGMLGATGGLNLCYQTNFAS 256
 Db 246 IINGREFCDVQNDANVDRIGYTRCYGMLGADPGSNLDCYNQRFDS 293

RESULT 8
 O04271 PRELIMINARY; PRT; 289 AA.
 AC O04271;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CHITINASE.
 GN CHIAO.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IR36;
 RA Yun C.-H., Lee B.P., Yun K.J., Eun M.Y.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001500; AAB58238.1; -
 DR HSSP; P23951; 2BAA.
 DR Mendel; 14790; Oryza; Chiao; 14790.
 DR InterPro; IPR000726; Glyco_hydro.19.
 DR Pfam; PF00182; Glyco_hydro.19; 1.
 DR ProDom; PD000574; Glyco_hydro.19; 1.
 DR PROSITE; PS00774; CHITINASE_19.2; 1.
 SQ SEQUENCE 289 AA; 31037 MW; 3EB53DF957B8FE72 CRC64;

Query Match 71.5%; Score 973.5; DB 10; Length 289;
 Best Local Similarity 74.4%; Pred. No. 6.6e-76;
 Matches 186; Conservative 19; Mismatches 38; Indels 7; Gaps 3;

QY 9 VCAA-----ALLAVAGAAAGGVSVITRSVYASMLPNRNSLCPARGFYTDAFIAA 64
 Db 38 VCSACRVPAALLAVAAW--RRQGVSVITQAVFNSMLPNRNSLCPARGFYTDAFIAA 95
 QY 65 NTFPGGTTGSA-DDIKRDLAFAFFGQTSHETGGTGRGAADQFQWGYCFKEEISKATSP 123
 Db 96 NSFRSARAGGAPSSRRRELAFFGQTSHETGGTGRGSSDQFQWGYCFKEEINKATSP 155
 QY 124 YGRGPIQLTGRSNDLAGRAIGKDLVSNPDVSTDAVVFRTAMFWMTAAGNKKPSCHV 183
 Db 156 YGRGPIQLTGSQYQAAGNALGLDLYGNPDVSTDAVVFRTAMFWMTAAGNKKASCHV 215
 QY 184 ALRRWPTAATDAGRVPGYGVITNIIINGLEGCMGRDANVDRIGYTRCYGMLGATG 243
 Db 216 ILGRWTPRGGTAGRVPGYGVITNIIINGLEGCMGRDANVDRIGYTRCYGMLGATG 275
 QY 244 GNLDCTQORN 253
 Db 276 SNLDCTQORN 285

RESULT 9
 Q43835 PRELIMINARY; PRT; 236 AA.
 ID Q43835
 AC Q43835;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
 DE ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE) (FRAGMENT).
 GN CHIAO OR CHPAL.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. DATURA; TISSUE=LEAF;
 RX MEDLINE=9808002; PubMed=9426596;
 RA Buchter R., Stromberg A., Schmelzer E., Kombrink E.;
 RT "Primary structure and expression of acidic (class II) chitinase in
 RT potato.";
 RL Plant Mol. Biol. 35:749-761(1997).
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-

22 AONAGSIIVTRELFEQMLSFRRNDVCPGKGGFTYDYDAFIAAANSFFPAFGTTGGDTARKKEMA 81

85 AFFGQTSHTTGGTGAADQFQWGGCFKEEISKATSPYYGGRGPQLTGRSNYDLAARAI 144

82 AFFGQTSHTTGGGAGT--FTGGYCFVRQIDQ--SERYGGRGPQLTGHQSNYERAGOGI 136

145 --GKDLVSNPDLVSDAVVSFRTAMFWMTAGNKPSPCHNVALRWTTAADAAGRVP 202

137 GVGQDLVNNPDLVATDPIISFXTAIWFNMTAQDNKPSCHNVIIGOWTTPSAADTAANRVP 196

203 YGVITNIINGGLECGMRNDANVDRIGYTRYCYGMLGTATGNNLDCYTORNEA 255

197 YGVITNIINGGLECGMPNTAVESRIGFYRRYCGMLNVTGENLDCNNORNEA 249

RESULT 11

Q43834 PRELIMINARY; PRT; 252 AA.

Q43834; ID

Q1-NOV-1996 (TReMBLrel. 01, Created)

01-NOV-1996 (TReMBLrel. 01, Last annotation update)

01-JUN-2001 (TReMBLrel. 17, Last annotation update)

CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).

CHIAO OR CHTA2.

Solanum tuberosum (Potato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

NCBI_Taxid=4113;

[1]

SEQUENCE FROM N.A.

STRAIN=CV. DATURA; TISSUE=LEAF;

MEDLINE=98088002; PubMed=9426596;

Bucher R., Stromberg A., Schmelzer E., Kombrink E.;

"Primary structure and expression of acidic (class II) chitinase in potato.";

Plant Mol. Biol. 35:749-761(1997).

-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

EMBL; U45969; BAB96341.1; --

HSSP; P23951; ZBAA.

Mandel; 14796; Soltu; chia0; 14796.

InterPro; IPR000726; Glyco_hydro_19.

Pfam; PF00182; Glyco_hydro_19; 1.

ProDom; PD000574; Glyco_hydro_19; 1.

PROSITE; PS00773; CHITINASE_19_1; 1.

PROSITE; PS00774; CHITINASE_19_2; 1.

Hydrolase; Glycosidase.

SEQUENCE 252 AA; 27491 MW; 2DC63CEB2C319B31 CRC64;

Query Match 60.4%; Score 822.5; DB 10; Length 252;

BestLocal Similarity 65.7%; Pred. No. 5.2e-63;

Matches 153; Conservative 28; Mismatches 45; Indels 7; Gaps 3;

25 AOGVGSVITRSVYASMLNDRNSLCPARGFTYDYDAFIAAANFTPGFTGTSADDIKRDLA 84

23 AONAGSIIVTRELFEQMLSFRRNDVCPGKGGFTYDYDAFIAAANSFFPAFGTTGGDTARKKEMA 82

85 AFFGQTSHTTGGTGAADQFQWGGCFKEEISKATSPYYGGRGPQLTGRSNYDLAARAI 144

83 AFFGQTSHTTGGGAGT--FTGGYCFVRQIDQ--SERYGGRGPQLTGHQSNYERAGOGI 137

145 --GKDLVSNPDLVSDAVVSFRTAMFWMTAGNKPSPCHNVALRWTTAADAAGRVP 202

138 GVGQDLVNNPDLVATDPIISFXTAIWFNMTAQDNKPSCHNVIIGOWTTPSAADTAANRVP 197

203 YGVITNIINGGLECGMRNDANVDRIGYTRYCYGMLGTATGNNLDCYTORNEA 255

198 YGVITNIINGGLECGMPNTAVESRIGFYRRYCGMLNVTGENLDCNNORNEA 250

```

RT "A new class II rice chitinase, Rcht2, whose induction by fungal
RT elicitor is abolished by protein phosphatase 1 and 2A inhibitor.";
RL Plant Mol. Biol. 37:523-534(1998).
DR EMBL; L40338; AAC37516.1; -.
DR HSP; P23951; 2BAA.
DR Mendel; 26889; Oryza; Chiao; 26889.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase.
FT NON_TER 1
SQ SEQUENCE 175 AA; 18969 MW; 489333BLBAFCBLFCE CRC64;

Query Match 59.8%; Score 814; DB 10; Length 175;
Best Local Similarity 83.4%; Pred. No. 1.8e-62;
Matches 146; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 82 DIAAFGGTSHETGGTGAADQFQWGYCFKKEISKATSPYYGRGPIQLTGRSNYDLA 141
DB 1 ELAAFFGGTSHETGGTGRSSDQFQWGYCFKKEINKATSPYYGRGPIQLTGRSNYQ 60
QY 142 RAIGKDLVSNPDVSTDAVSFRTAMFWMTAQGNKPSCHNVALRWTTAATTAAGRVP 201
DB 61 NALGLDLVGNPDVSTDAVSFKTAIWMTAQGNKPSCHDVILGWTFSAADTAAYRVP 120
QY 202 YGVITNIINGLEGCGMRDANVDRIYGYTCYCGMLGTATGNCNLCYTORNFA 256
DB 121 GYDGTNIINGGIECGVGONDANVDRIYKRYKRYCDMLGTYGNCNLCYQNRNFA 175

RESULT 14
O82552 PRELIMINARY; PRT; 253 AA.
AC O82552;
DT 01-NOV-1998 (TrEMBLrel. 03, Created)
DT 01-NOV-1998 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE CLASS II.
GN CHIAO OR CACH12.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HANBYUL; TISSUE=LEAF;
RA Hwang B.K., Hong J.K., Kim Y.J.;
RT "Molecular cloning and characterization of a pathogen-induced gene
RT encoding a basic class II chitinase from Capsicum annuum.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091235; AAC36359.1; -.
DR HSP; P23951; 2BAA.
DR Mendel; 33139; Capan; Chiao; 33139.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
SQ SEQUENCE 253 AA; 27768 MW; F464515215B62251 CRC64;

Query Match 59.4%; Score 808.5; DB 10; Length 253;
Best Local Similarity 59.4%; Pred. No. 8.3e-62;
Matches 151; Conservative 32; Mismatches 64; Indels 7; Gaps 3;

QY 4 FAALAVCAALLLAVAAGAAAGAGVGSVITRSVYASMLFNDRNSLCFARGFTYDAFIA 63
DB 3 FSVSPVALSCLFELFLITLITLQNTGSIYTRDLFERMLSRNNAACPGKGYTFEAFITA 62
QY 64 ANTFPGFGTGSADDIKRDLAFFGQTSHETGGTGAADQFQWGYCFKKEISKATSPY 123

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QY      230  YTRYCGMIGTATGGLNDCYTORNF 254
      :| ||| :| | |||| | :| |
Db      240  FYKRYCDILKIGYGNLDCANOOHF 264

Search completed: May  3, 2002, 13:46:59
Job time: 883 sec

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db	63	ANSFPAGTGDNTARKKEAAAFGCTSHETNGRAGT---PNGCYCFVRQDQ--SDRY	117
QY	124	YGRGPQLTGRSNDYLAGRAI--GKDLVSNPOLVSTDADVVFRTAMFWKRAQGNKPSCH	181
Db	118	YGRGPQLTGRSRYERAGRIGYGDLVNPDPKATNPVISEKTAIWFMTAADDNKPSC	177
QY	182	NVALRWTPPTAATAAGRYPGCVITNIINGGIECGMGRENDANVDRIGYTYRCGMGLTA	241
Db	178	DVIIGRWKPSPADRSANRPYGVITNIINGGIECGKGRNGAVESRIGFYKRYCGMLNVP	237
QY	242	TGGNLDCYTGQNFPA	255
Db	238	TGNNLDCYNQKNEA	251

Search completed: May 3, 2002, 13:46:59
Job time: 883 sec

RESULT	15	
ID	Q42515	PRELIMINARY; PRT; 264 AA.
AC	Q42515;	
DT	01-NOV-1996 (TREMblrel. 01, Created)	
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)	
DT	01-JUN-2001 (TREMblrel. 17, Last annotation update)	
DE	CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-D-GLUCOSAMINIDASE).	
DE	CHIA2 OR CH12.2.	
GN	Arachis hypogaea (Peanut).	
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eucosids I; Fabales; Fabaceae; Papilionoideae; Arachis.	
OX	NCBI_TaxID=3818;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV. NC 4;	
EX	MEDLINE=96178874; PubMed=8616259;	
RA	Kellmann J.W., Kleinow T., Engelhardt K., Philipp C., Wegener D.,	
RA	Schell J., Schreier P.H.;	
RT	"Characterization of two class II chitinase genes from peanut and	
RT	expression studies in transgenic tobacco plants.";	
RL	Plant Mol. Biol. 30:351-358(1996).	
CC	!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.	
CC	EMBL; X82330; CAA57774.1; ..	
DR	HSSP; P23951; 2BAA.	
DR	Mendel; 1624; Arach;Chia2;1624.	
DR	InterPro; IPR000726; Glyco_hydro.19.	
DR	Pfam; PF00182; Glyco_hydro.19; 1.	
DR	ProDom; PD000574; Glyco_hydro.19; 1.	
DR	PROSITE; PS00773; CHITINASE.19; 1.	
DR	PROSITE; PS00774; CHITINASE.19_2; 1.	
KW	Hydrolase; Glycosidase.	
SO	SEQUENCE 264 AA; 28924 MW; CCBI3C590ADB5D8A CRC64.	

Query Match	59.1%	Score	805.5	DB	10	Length	264
Best Local Similarity	57.4%	Pred. No.	1.6e-61				
Matches	152	Conservative	35	Mismatches	63	Indels	15
Gaps							
Qy	3	RF	AALVCA	RAALLI	NAAGAA	GGVSV	VT
Db	2	KC	NEFTT	FTI	LV	IQAL	CA
Qy	63	AA	NTFP	GGT	GT	SADD	--
Db	62	AA	RAFP	AF	AGT	GT	--
Qy	116	SK	ANSP	----	----	----	----
Db	120	CD	STQA	CP	CK	QY	YGR
Qy	170	WM	TAGN	KPS	CHN	VAL	RW
Db	180	WM	TAGN	KPS	CHN	VAL	RW

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:30:29 ; Search time 117.39 Seconds
(without alignments)
203.814 Million cell updates/sec

Title: US-09-534-229C-2
Perfect score: 1792
Sequence: 1 MSTLRARCATAVLAIVLAAA.....YGNLDCYNQLSFNVGLAAQ 323

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1792	100.0	323	22 AAB11488	Wheat chitinase pr
2	1294.5	72.2	319	22 AAB11489	Wheat chitinase pr
3	1290	72.0	318	20 AAW98079	Rye chitinase-like
4	1265	70.6	298	20 AAW98080	Rye chitinase-like
5	1230	68.6	336	13 AAR29019	RCHI0 chitinase pr
6	1230	68.6	336	16 AAR67969	Rice chitinase. o
7	1230	68.6	336	22 AAB67444	Amino acid sequenc
8	1177.5	65.7	324	12 AAB13275	Tobacco intracellu
9	1177.5	65.7	324	18 AAW31297	Nicotiana sp. intr
10	1177.5	65.7	324	21 AAB07513	Amino acid sequenc
11	1170	65.3	329	12 AAB15841	Basic chitinase 48

12	1163.5	64.9	292	18 AAW24554	Chitinase. Cucurb
13	1161	64.8	331	12 AAB11305	Chitinase encoded
14	1160	64.7	317	17 AAW00186	American elm chiti
15	1142.5	63.8	328	13 AAR20822	Sequence of endoch
16	1141.5	63.7	329	15 AAR56860	Endochitinase prec
17	1081.5	60.4	303	13 AAR20820	Sequence of a 302
18	1055	58.9	266	15 AAR52577	Chitinase G. Hord
19	1052.5	58.7	328	19 AAW64776	Floral organ-speci
20	930	51.9	2466	20 AAY05844	Banana ripening fr
21	879	49.1	243	20 AAW90169	C. ensiformis chit
22	827	46.1	259	21 AAB18902	A maize chitinase
23	818.5	45.7	254	12 AAB13274	Petunia extracellu
24	818.5	45.7	254	18 AAW31296	Petunia hybrida ex
25	818.5	45.7	254	21 AAB07512	Amino acid sequenc
26	809	45.1	253	16 AAR76714	Tobacco endochitin
27	798	44.5	256	22 AAB11487	Wheat chitinase pr
28	795	44.4	439	13 AAR28150	Sugar beet chitina
29	790	44.1	252	20 AAW98081	Rye chitinase-like
30	786	43.9	230	20 AAW98082	Rye chitinase-like
31	779.5	43.5	250	16 AAR76713	Wild tomato endoch
32	779.5	43.5	252	21 AAB18903	A maize chitinase
33	775.5	43.3	253	16 AAR76712	Wild tomato endoch
34	774	43.2	284	21 AAB18905	A maize chitinase
35	770.5	43.0	272	21 AAG28415	Arabidopsis thalia
36	770.5	43.0	280	21 AAG28414	Arabidopsis thalia
37	707.5	39.5	372	22 AAB28788	Protein encoded by
38	644.5	36.0	155	21 AAB18906	Amino acid sequenc
39	633	35.3	271	21 AAB18904	Amino acid sequenc
40	633	35.3	271	21 AAB18936	Sugar beet chitina
41	597.5	33.3	268	13 AAR28147	A maize chitinase
42	595.5	33.2	281	21 AAB18894	Sugar beet chitina
43	584	32.6	264	13 AAR28145	Sugar beet chitina
44	492	27.5	813	21 AAG53657	Arabidopsis thalia
45	480.5	26.8	328	21 AAB18899	A maize chitinase

ALIGNMENTS

RESULT 1
AAB11488
ID AAB11488 standard; protein; 323 AA.
AC AAB11488;
XX
XX 02-MAR-2001 (first entry)
XX Wheat chitinase protein homologous to rye chitinase.
XX
XX Wheat; chitinase; low temperature expression; hardened; plant;
XX snow mould resistance; psychophilic plant pathogen; rye.
XX Triticum aestivum.
XX
XX JP2000270866-A.
XX 03-OCT-2000.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX 25-MAR-1999; 99JP-0081694.
XX
XX (HOKK-) HOKKAIDO NAGOY SHIKENBACHO.
XX WPI; 2001-027417/04.

PT New low temperature expression chitinase gene for producing a plant
grade highly resistant to psychophilic plant pathogenic microbes
XX
XX Claim 4; Fig 2; 11pp; Japanese.
XX This invention describes novel wheat chitinase genes. The invention also
CC describes a method for the isolation of a low temperature expression

PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.
 PT and for treating tumours

XX Claim 10; Fig 21a; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
 CC CH99 preprotein. The mature protein, which is also claimed, is a
 CC chitinase-like protein that has chitinase (antifungal) and
 CC antifreeze activities. CH99 cDNA (see AAX24889) was obtained by
 CC isolating mRNA from rye plants grown at low temperatures in the
 CC absence of pathogens or other stresses, i.e. under conditions when
 CC only chitinases with antifreeze activity would be expressed. CH99
 CC and CH46 (see AAW98081-82) have been cloned and expressed in
 CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
 CC The chitinase-like antifreeze proteins can be used: to increase
 CC freezing tolerance of plants and microorganisms; to increase field
 CC survival of plants, animals and microorganisms exposed to sub-zero
 CC temperatures; to inhibit ice recrystallisation in biological
 CC materials or foods; for cryopreservation and hypothermic protection
 CC of cells, embryos, tissues etc. (particularly human platelets); and
 CC to kill tumour cells. They are also used to inhibit initiation and
 CC progression of diseases or spoilage caused by low temperature
 CC pathogens (particularly fungi) in plants, frozen foods and any
 CC cryopreserved biological material. The signal peptide can be used
 CC to direct protein secretion in transgenic organisms or expression
 CC systems.

XX Sequence 318 AA;

Query Match 72.0%; Score 1290; DB 20; Length 318;
 Best Local Similarity 71.2%; Pred. No. 1.1e-101;
 Matches 223; Conservative 34; Mismatches 48; Indels 8; Gaps 1;

QY 12 VLAVLAAAVTPTAAEOCGSAGGAKADCLCCSOFGCGTTSYCGPRCQSQCTGCGG 71

Db 5 vvvamaafavsahaeqcgsgagatcpcnclccskfscgstseycgdcgqscnrcgg 64

QY 72 -----GGGVASIVSRDLFRFLHNRDAACLAGFYTYDAFLAAGAFPAFGTGD 123

Db 65 tppvptptggvgssliisldqmlhnrdaaclakgfyngafiaaansfgfattg 124

QY 124 LDRKREVAFFGCTSHETGGWPTAPDGPFSWGYCFKQBGSPSPSYCDQADWPCAPGK 183

Db 125 tdrvkrevaafagtshtgttgwptadgyswgycfngergapsdycspssqwpcapgk 184

QY 184 QYXGRGPIQLTHNYNGPAGRAIGVDLLNPDILVATDPTVAFKTAIWFWMTOSNKPSC 243

Db 185 kyfgrgpiqisynynygpagraigtldlnnpdlvatdatsvfktafwmtpskps 244

QY 244 DVTGLWTPARDASAGRVPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCIDIFG 303

Db 245 dvtgrwspsgaadaagrvpgygvitnilinglecggrgqdarvadrigfykrycdilgvs 304

QY 304 YGNLDCYNOLSF 316

Db 305 ygndldcynprpf 317

RESULT 4

AAW98080

ID AAW98080 standard; Protein; 298 AA.

XX AAW98080;

AC AAW98080;

DT 21-JUN-1999 (first entry)

XX Rye chitinase-like protein CH99.

XX CH99; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.

XX Secale cereale.

XX WO9906565-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

XX N-PSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
 PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.
 PT and for treating tumours

XX Claim 10; Fig 21d; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
 CC CH99 mature protein. It lacks the 20-amino acid signal peptide
 CC of the preprotein (see AAW98079), which is also claimed. Mature CH99
 CC is a chitinase-like protein that has chitinase (antifungal) and
 CC antifreeze activities. CH99 preprotein cDNA (see AAX24889) was
 CC obtained by isolating mRNA from rye plants grown at low temperatures
 CC in the absence of pathogens or other stresses, i.e. under conditions
 CC when only chitinases with antifreeze activity would be expressed.
 CC CH99 and CH46 (see AAW98081-82) have been cloned and expressed in
 CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
 CC The chitinase-like antifreeze proteins can be used: to increase field
 CC freezing tolerance of plants and microorganisms; to increase field
 CC survival of plants, animals and microorganisms exposed to sub-zero
 CC temperatures; to inhibit ice recrystallisation in biological
 CC materials or foods; for cryopreservation and hypothermic protection
 CC of cells, embryos, tissues etc. (particularly human platelets); and
 CC to kill tumour cells. They are also used to inhibit initiation and
 CC progression of diseases or spoilage caused by low temperature
 CC pathogens (particularly fungi) in plants, frozen foods and any
 CC cryopreserved biological material.

XX Sequence 298 AA;

Query Match 70.6%; Score 1265; DB 20; Length 298;
 Best Local Similarity 72.7%; Pred. No. 1.3e-99;
 Matches 216; Conservative 32; Mismatches 41; Indels 8; Gaps 1;

QY 28 EOCGSQAGGAKADCLCCSOFGCGTTSYCGPRCQSQCTGCGG-----GGGVASI 79

Db 1 eqcsgaggaatcpcnclccskfscgstseycgdcgqscnrcgtpvptptggvgss 60

QY 80 VSRDLFRFLHNRDAACLAGFYTYDAFLAAGAFPAFGTGDTRKREVAFFGCT 139

Db 61 isqslfdqmlhnrdaaclakgfyngafiaaansfgfattgtdrvkrevaafagts 120

QY 140 HETGGWPTAPDGPFSWGYCFKQBGSPSPSYCDQADWPCAPGKYXGRGPIQLTHNY 199

Db 121 hettggwptadgyswgycfngergapsdycspssqwpcapgkkyfgrgpiqisyn 180

QY 200 GPAGRAIGVDLLNPDILVATDPTVAFKTAIWFWMTOSNKPSCHDVITGLTPTARDSAA 259

Db 181 gpagraigtldlnnpdlvatdatsvfktafwmtpskpsshdvtgrwspsgaada 240

QY 260 GRVPGYGVITNVIINGTECGMGQNDKVADRIGFYKRYCIDIFGIGNLDCYNOLSF 316

Db 241 grvpgygvitnilinglecggrgqdarvadrigfykrycdilgvsygndldcynprpf 297

QY 116 PAFCTTGDLTRKREVAFFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
 Db 118 p9faagadadnkrrevaafagtshtettggwatapdgytwgcyfkeengagapdyccqs 177
 QY 175 ADWPCAPGQYYGRGPIQLTHNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
 Db 178 aqwpcaagkxygrgpiqlsynfygpaggaigadllgdpdlvasdatvstafwmt 237
 QY 235 TQSNKPSCHDVITGLWTPARTASAGRPVGYGVINNVINGGIECGMGONDKVADRIGFYK 294
 Db 238 pqsppkpsnavatgwtbsadddragrvpygyvtnilngglecghgeddriadrigfyk 297
 QY 295 RYCDIFGIGYGNLDCYNQ 313
 Db 298 rycdilgvsyganldcysq 316

RESULT 7
 AAB67444
 ID AAB67444 standard; Protein; 336 AA.
 XX AAB67444;
 AC AAB67444;
 DT 15-MAY-2001 (first entry)
 DE Amino acid sequence of a rice chitinase designated RCH10.
 KW Disease resistance protein; xa21; RKK gene; transgenic plant; chitinase;
 KW Xanthomonas; plant pathogen; Brill protein; RCH10 protein.
 OS Oryza sp.
 PN WO200109283-A2.
 XX 08-FEB-2001.
 XX 28-JUL-2000; 2000WO-US20714.
 XX 28-JUL-1999; 99US-0363313.
 PA (REGC) UNIV CALIFORNIA.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 PI Ronald P, He Z, Chory J, Lamb C, Li J;
 DR WPI; 2001-159858/16.
 DR N-PSDB; AAF54983.

Chimeric plant receptors comprising a polynucleotide encoding a RKK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses to pathogens -
 XX Disclosure; Page 45-46; 47pp; English.
 XX The present sequence represents a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Brill protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp.. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to confer desired traits on essentially any plant.
 XX Sequence 336 AA;

Query Match 68.68; Score 1230; DB 22; Length 336;
 Best Local Similarity 69.34; Pred. No. 1.4e-96;
 Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

QY 4 LRARCATAVLAVLWIAAAAVTPATAEQCQSQAGGAKACDCLCCSQPFGCGTSTDYCGPRCQ 63
 Db 1 mralavavmvarpfilaav---haeqcgsgagavcpnclocsqfgwgsgstdycgagcq 57
 QY 64 SQCT-----GCGGGGGVASIVSRDLFEFLHNRDAACLARGFVTDYDAFLAAAGAF 115
 Db 58 sqcsrlrrrrpdasggsgvasivsrslfdlmlhndaacpasnftydafvaasaf 117
 QY 116 PAFGTGDLIDTRKREVAFAFFGQTSHTTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
 Db 118 p9faagadadnkrrevaafagtshtettggwatapdgytwgcyfkeengagapdyccqs 177
 QY 175 ADWPCAPGQYYGRGPIQLTHNYNGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
 Db 178 aqwpcaagkxygrgpiqlsynfygpaggaigadllgdpdlvasdatvstafwmt 237
 QY 235 TQSNKPSCHDVITGLWTPARTASAGRPVGYGVINNVINGGIECGMGONDKVADRIGFYK 294
 Db 238 pqsppkpsnavatgwtbsadddragrvpygyvtnilngglecghgeddriadrigfyk 297
 QY 295 RYCDIFGIGYGNLDCYNQ 313
 Db 298 rycdilgvsyganldcysq 316

RESULT 8
 AAR13275
 ID AAR13275 standard; Protein; 324 AA.
 XX AAR13275;
 AC AAR13275;
 DT 14-OCT-1991 (first entry)
 DE Tobacco intracellular chitinase.
 KW fungal resistance; phytopathogen.
 XX Nicotiana tabacum Samsun NN.
 EH Key Location/Qualifiers
 FT Peptide 1..23
 FT Protein 24..324
 FT /label= intracellular chitinase
 XX EP440304-A.
 PN 07-AUG-1991.
 PD 30-JAN-1991; 91EP-0200191.
 PR 30-JAN-1990; 90NL-0000222.
 PA (MOGE-) MOGEN INT NV.
 PA (UYLE-) RIJKSUNIV TE LEIDEN.

XX Cornelissen BJ, Melchers LS, Meulenhoff EJ, Van Roekel JS;
 XX Sela-Buurlage MB, Vloemans AA, Woloshuk CP, Bol JF;
 XX WPI; 1991-232019/32.
 DR N-PSDB; AAQ12898.
 XX Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targeted to apoplasts
 XX Example 4; Fig 2; 55pp; English.

XX The sequence from which this amino acid was deduced was isolated from a N.tabacum cDNA library following screening with a partial tobacco intracellular chitinase clone. The protein sequence appears twice in the specification but in one (not the one given in this

CC file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7,
CC -6, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266,
CC 274, 286 are translated as Ile.
CC See AAQ12897-Q12900.

XX
XX SQ Sequence 324 AA;

Query Match 65.7%; Score 1177.5; DB 12; Length 324;
Best Local Similarity 64.2%; Pred. No. 3.9e-92;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;

QY 8 CATAVLAVLIAAAVTPATAECGSGAGKACADCLCCSQFGTSDYCGP-RCQSQC 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 4 ckftalsllfslillsaaecqsgaggarcasglccskfgwcnntndycpgnccsqc 63

QY 67 TG--CGGGGGGVASIVSRDLFERFLLRNDAACTARGFTTYDAFLAACAFPAFTTGDL 124
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 64 pggtpgggdlgsilssmfdqlkhrudnacgkgfyfnafinaarsifpgftsgdt 123

QY 125 DTRKEVAARFGQTSHETTGWPTAPDPFESWGVCFKCEQGSPSYCDQSADWPcapgk 184
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 124 tarkrelaaffaqtshttgwatpdgyawgycwlrceqspgdyctpsgawpcapgrk 183

QY 165 YVGPGPIQLTHNYNGPAGRAIGVDLLNNPDIAVDPTVAFKIALFWMTTSNKPSCHD 244
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 164 yfgrgpidishynyvpcgraigvdlnnpdivatdpvisfklsalwfmtpsgpkschd 243

QY 245 VTGLWTPTARSAGRVPYGVIINVTINGGTECGNQDNDKVDRIGFYKRYCDIFIGY 304
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 244 vliqrwpssadraanrlpgfvitniingiecdrgtdrvqdrrgfyrriyccslgvsp 303

QY 305 GNMLDCYNQLSFNVGL 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 304 gdnldcgndrsfgngl 319

RESULT 9
AAW31297
ID AAW31297 standard; Protein; 324 AA.
XX AC AAW31297;
XX DT 11-MAR-1998 (first entry)
XX DE Nicotiana sp. intracellular chitinase protein.
XX Intracellular chitinase; antifungal; transgenic plant; synergism;
KW beta-1,3-glucanase gene; tobacco.
XX OS Nicotiana sp.
XX Key Location/Qualifiers
FH 1..23 /label= signal_peptide
FT Peptide
FT Protein 24..324
FT /note= "intracellular protein"
FX US5670706-A.
FN
XX PD 23-SEP-1997.
XX PF 19-APR-1993; 93US-0047413.
XX PR 29-JAN-1991; 91US-0647831.
XX PA (MOGE-) MOGEN INT NV.
XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX Bol JF, Cornelissen BJC, Linthorst HJM, Melchers LS;
PI Meulenhoff EJS, Sela-buurlage MB, Van ROEKEL JSC;
PI Vloegmans AA, Woloshuk PI;
XX

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PF 18-FEB-1997; 97US-0801563.
XX
XX 19-APR-1993; 93US-0047413.
PR 29-JAN-1991; 91US-0647831.
XX
XX (OYLE-) RIJKSUNIV LEIDEN.
PA (MOGE-) MOGEN INT NV.
XX
XX Cornelissen BJC, Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
PI Vloemans AA, Woloshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
XX
XX WPI: 2000-498214/44.
DR N-PSDB; AAA58910.
XX
XX New transgenic plants expressing chitinase and glucanase have improved
PT resistance against pathogenic fungi, particularly against Alternaria
PT alternata or Fusarium oxysporum f. sp. lycopersici -
XX
XX Example 4; Fig 2A-B; 42pp; English.
PS
XX The present sequence represents an extracellular chitinase. The
CC specification describes transgenic plants which express a chitinase
CC gene and a glucanase gene. The expression of the chitinase and
CC beta-1,3-glucanase genes produces an antifungal effect. The transgenic
CC plants are useful for improving plant resistance to pathogenic fungi.
CC The recombinant polynucleotides and the process are useful for
CC producing fungal resistant plants.
XX
XX Sequence 324 AA;
SQ
Query Match 65.7%; Score 1177.5; DB 21; Length 324;
Best Local Similarity 64.2%; Pred. No. 3.9e-92;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;

QY 8 CATAVLVAAVLAATAAEQCSQAGGAKCADCICCSQFGCGTSDYCGP-RCQSQC 66
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 ckftalsllfslillsaeeqcsqaggarpcsglccskfsgcgtndygcpgnwgscq 63

QY 67 TG--CGGGGGVASIVSRDLFERFLHRNDAACLARGFYDYDAFLAAGAFPAFGTGL 124
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 ppgtpppggdslsissmfdqmlkhrndnacqgkfysynafinaarsfpfgtsagt 123

QY 125 DTRKREVAAPFGQTSHTTGGWPTAPDPGFSWGYCFKQEGSPSYCDQADPFCAPGKQ 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 tarkreiaafagtshtetggwatapdgyawycwlrqcsqdyctpsgqwpcabgrk 183

QY 185 YGSGPIQLTHNINYPAGRAIGVDLLNPNLVATDPTVAEKTALWFWMTQSNKPSCHD 244
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 yfgrgpiqishnynypcgraigvdlldnnpdvatdpvisfksalwfmwmpqspkpschd 243

QY 245 VITGLWPTARSDAAGRPVGYGVITNVINGIECGMGQNDKVDADRIGFYKRYCDIFGIGY 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 viilgrwpsaadraanrlpfgvltningglecgrgtdsrvgdrigfyrriycsilgvsp 303

QY 305 GNNLDCYNQLSFNVGL 320
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 gdnldcgnqrsfngl 319

RESULT 11
ID AAR15841
XX AAR15841 standard; Protein; 329 AA.
XX
XX AAR15841;
AC AAR15841;
XX
XX 19-MAR-1992 (first entry)
DT
XX Basic chitinase 48 from clone lambdaCHN17.
XX
XX Vacuole; targeting; chitinase; glucanase; signal; resistance;
KW pharmaceutical; hormones; expression; secretion; extracellular.
XX
XX

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OS Nicotiana tabacum L. C.V. Havana 425.
XX
XX Key Location/Qualifiers
FH 1..148
FT Region /label= exon1_prod.
FT 149..199
FT Region /label= exon2_prod.
FT 200..329
FT Region /label= exon3_prod.
FT 318..329
FT Peptide /label= sig_peptide
FT /note= "used as vacuole targeting peptide"
XX
XX EP462065-A.
PN
XX 18-DEC-1991.
PD
XX 06-JUN-1991; 91EP-0810430.
PF
XX 15-JUN-1990; 90CH-0002007.
PR
XX (CIBA ) CIBA GEIGY AG.
PA
XX Bollier T, Nauhaus JM, Ryals J;
PI
XX WPI: 1991-371028/51.
DR N-PSDB; AAQ15147.
XX
XX DNA sequence encoding vacuole targeting peptide - esp. signal
PT region of tobacco chitinase or glucanase gene, and derived
PT recombinant DNA, vectors, etc. functional in plants
XX
XX Disclosure; Page 64-68; 81pp; English.
PS
XX Attachment of the signal peptide ensures occlusion of expressed
CC prod. in the vacuole while elimination of the signal peptide from
CC a sequence normally contg. it ensures that the expressed product
CC is secreted into the extracellular space, rather than retained in
CC the vacuole. Recombinant DNA may contain a structural gene which
CC protects the plant, e.g. resistance to pathogens, herbicides,
CC insecticides, biocides, environmental stress, etc.; leads to
CC increased prodn. of proteins, carbohydrates, etc.; or encodes for
CC pharmaceuticals such as hormones or immunomodulators.
CC See also AAQ15146-50 and AAQ15330-35.
XX
XX Sequence 329 AA;
SQ
Query Match 65.3%; Score 1170; DB 12; Length 329;
Best Local Similarity 63.2%; Pred. No. 1.7e-91;
Matches 203; Conservative 44; Mismatches 66; Indels 8; Gaps 2;

QY 8 CATAVLVAAVLAATAAEQCSQAGGAKCADCICCSQFGCGTSDYCGP-RCQSQC 66
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 ckftalsllfslillsaeeqcsqaggarpcsglccskfsgcgtndygcpgnwgscq 63

QY 67 TG-----CGGGGGVASIVSRDLFERFLHRNDAACLARGFYDYDAFLAAGAFPAFG 119
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 ppgtppptpppggdslsissmfdqmlkhrndnacqgkfysynafinaarsfpfg 123

QY 120 TTGDLDTKREVAAPFGQTSHTTGGWPTAPDPGFSWGYCFKQEGSPSYCDQADPFC 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 tsqdtarkreiaafagtshtetggwatapdgyawycwlrqcsqdyctpsgqwp 183

QY 180 AFGKQYGRGPIQLTHNINYPAGRAIGVDLLNPNLVATDPTVAEKTALWFWMTQSNK 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 apgrkyfgrgpiqishnynypcgraigvdlldnnpdvatdpvisfksalwfmwmpcp 243

QY 240 PSCHDVITGLWPTARSDAAGRPVGYGVITNVINGIECGMGQNDKVDADRIGFYKRYCDI 299
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 pschdvilgrwpsaadraanrlpfgvltningglecgrgtdsrvgdrigfyrriycsi 303

QY 300 FGIGYGNLDCYNQLSFNVGL 320

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Db 184 capgrkyfgrgpiqishnnygpcgragvdlonpdlvatdpvisksalwfmtpqs 243
 QY 238 NKPSCHDVTGLWTTARDASAGRPVGVITNVINGIECGMGQNDKVADRIGVKKRYC 297
 Db 244 pkpschdvilgrwpsagdraanripvgfviitniingiecggrdsrvdgrigfrryc 303
 QY 298 DIFGIGYGNLDCYNOLSFNVL 320
 Db 304 silgvsppgnldcgoqrsfngl 326

RESULT 14
 AAW00186
 ID AAW00186 standard; Protein; 317 AA.
 XX
 AC AAW00186;
 XX
 DT 18-OCT-1996 (first entry)
 XX
 DE American elm chitinase-like protein.
 XX
 KW Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi;
 KW dutch elm disease; E. coli; chitinase-like protein;
 KW fungal infection.
 XX
 OS American elm.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "signal peptide"
 FT 22..317
 FT /note= "Mature chitinase-like protein"
 XX
 XX US5539095-A.
 XX
 PD 23-JUL-1996.
 XX
 PF 04-AUG-1994; 94US-0286020.
 XX
 PR 04-AUG-1994; 94US-0286020.
 XX
 XX (UNMS) UNIV MICHIGAN STATE.
 PA
 XX Hajela RK, Sticklen MB;
 PI
 XX WPI: 1996-353879/35.
 DR
 DR N-PSDB; AAT33325.
 XX
 XX Isolated chitinase gene derived from an American elm - used to
 PT obtain prods. for inhibiting fungal infection of plants
 PT
 XX Claim 1; Fig 1; 12pp; English.
 PS
 XX This sequence is encoded by the cDNA clone pHS2, and represents a protein
 CC having chitinase-activity derived from american elm. This protein
 CC inhibits the fungus Ophiostoma ulmi, the causative agent of dutch
 CC elm disease. The clone pHS2 may be used to transform E. coli cells
 CC for the recombinant production of the chitinase-like protein. The
 CC protein may be used in a composition to inhibit fungal infection of
 CC elm trees.
 XX
 SQ Sequence 317 AA;

Query Match 64.7%; Score 1160; DB 17; Length 317;
 Best local Similarity 65.8%; Pred. No. 1.2e-90;
 Matches 204; Conservative 33; Mismatches 71; Indels 2; Gaps 1;
 QY 11 AVLAVVLAATAATPATAECGSGAGGAKCADCICCSQFCGTTSDYCGPRCQSQTGCG 70
 Db 5 alttisllisiqgwaecgsgagavcpvlgccskfwcgystneycgdcgcsqcg--g 62
 QY 71 GGGGGVASIVSRDLFFRFLHNRNDAACLAGFYTYDAFLAAGAFPAFTGTDLDTRKRE 130

Db 63 sgsddigglissafndmlkhrndggcpakgfytydafiaaakafpafgstgddttrkre 122
 QY 131 VAAFTGQTSHTTGWPTAPDGFPSWGYCFKQEGSPSPSYCDQADWPCAPKQYYGRGP 190
 Db 123 iaafigtshettgwasapdgpyswgycynreqppssdycsfptwpcasgkryfgrgp 182
 QY 191 IOLTHNYYGPAGRAIGVDLNNPDLVATDPVAFKTAIFWFWMTTOSNKPSCSHDVITGLW 250
 Db 183 iglswynygcgraignallnnpdlvatdpvisfktalwfmtpdspkpschdvtgrw 242
 QY 251 TPTARDSAAGRPVGVITNVINGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNLDC 310
 Db 243 spsgtdqsagravgvviitniingiecgkgqvpqvdvrigfkyrycdilrrygggnldc 302
 QY 311 YNOLSFNVL 320
 Db 303 ynqrpfgngl 312

RESULT 15
 AAR20822
 ID AAR20822 standard; Protein; 328 AA.
 XX
 AC AAR20822;
 XX
 DT 16-MAY-1992 (first entry)
 XX
 DE Sequence of endochitinase precursor.
 XX
 KW Pest-resistant plant; transformed plant; fungi; insect; bacteria;
 KW nematode.
 XX
 OS Tomato and tobacco.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= signal
 FT Peptide 25..69
 FT /label= cleavage
 XX
 PN WO9201792-A.
 XX
 PD 06-FEB-1992.
 XX
 PF 24-JUL-1991; 91WO-FR00607.
 XX
 PR 24-JUL-1990; 90FR-0009460.
 XX
 XX (SNFI) SANOFI SA.
 PA (ERAP) SOC NAT ELF AQUITAINE.
 XX
 XX Dubois M, Grison R, Leguay JJ, Pignard A, Toppan A;
 PI
 XX WPI: 1992-064950/08.
 DR N-PSDB; AAQ21193.
 DR
 XX New recombinant protein with endo chitinase activity - also DNA
 PT encoding it and plants which express it, resistant to fungi,
 PT insects, bacteria and nematodes.
 XX
 PS Example; Fig 4; 82pp; French.
 XX
 XX The inventors claim a new recombinant gene which codes for a protein
 CC with endochitinase activity, or its precursor (see AAQ21007). The
 CC coding part of the gene contains at least the 5' part of DNA for
 CC tomato endochitinase and at least the 3' part of DNA for the tobacco
 CC enzyme (DNA can be genomic or cDNA, but at least one intron is pref.
 CC present). The recombinant gene includes the 35S promoter of
 CC cauliflower mosaic virus plus the terminator from the nopaline
 CC synthase gene of Agrobacterium tumefaciens.
 XX
 SQ Sequence 328 AA;

Tue May 7 10:52:15 2002

us-09-534-229c-2.rag

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Query Match      63.8%; Score 1142.5; DB 13; Length 328;
Best Local Similarity 60.4%; Pred. No. 3.7e-89;
Matches 194; Conservative 54; Mismatches 66; Indels 7; Gaps 3;

QY 7 RCATAVLAVLAAAVTPATAEQGSGAGAKACDLCCSQFQFCGTTSDYCGP-RQSQ 65
Db 3 rtskltfslflslvllsaalaqncsgggkvcasggccskfgwcgntndhcgsgncsq 62
QY 66 CTGCGGG-----GGVASIVSRDLFERFLHRNDAACILAR-GFYTYDAFLAAAGAFPAFG 119
Db 63 cp9ggp9p9pvtgtdlgsvlsnsmfdqmlkhrnenscggknnfyynafitaarsfpqfg 122
QY 120 TTGDLDTKKREVAFFGQTSHETGGWPTAPDGFPSWGYCFKQEGSPSPSYCDQSADWPC 179
Db 123 tsgdinarkreiaafadtshettggwpsapdpfawgyctlrergnp9gycspssqwp 182
QY 180 AFGKQYGRGPQLTHNKNYPAGRAIGVDLLNPNDLVATDPVIAFKTAIWFWMTTQSNK 239
Db 183 apgrxyfgrbpqishnyny9pcraigvdl1nnpdlvatdpvisfktaiwfwmtpqspk 242
QY 240 PSCHDVITGLWTPRTARDSAAGKVPQYGVITNVINGIECGMGQNDKVADRIGFYKRYCDI 299
Db 243 pschdvliigrwnpsagdrsanrlp9fgvtnlingglecgrgndurvgdrigfyrtycgi 302
QY 300 FGIGYGNLDCYNQLSPNVGL 320
Db 303 lqvsp9dnldcgnqrsfgnql 323
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Search completed: May 3, 2002, 18:30:30
Job time: 7549 sec

Tue May 7 10:52:16 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:43:02 ; Search time 79.44 Seconds
(without alignments)
91.498 Million cell updates/sec

Title: US-09-534-229C-2
Perfect score: 1792
Sequence: 1 MSTLRACATAVLVAAVLA... YGNLDCYNQLSFNVGLAAQ 323

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1230	68.6	336	1	US-07-704-288C-3
2	1230	68.6	336	1	US-08-093-372-2
3	1230	68.6	336	1	US-08-379-259-3
4	1177.5	65.7	324	1	US-08-047-413-11
5	1177.5	65.7	324	3	US-08-229-050-11
6	1177.5	65.7	324	3	US-08-801-563-11
7	1176.5	65.7	310	4	US-07-791-931-6
8	1167	65.1	310	1	US-07-704-288C-6
9	1167	65.1	310	1	US-08-379-259-6
10	1141.5	63.7	329	2	US-08-475-427-13
11	1141.5	63.7	329	2	US-07-842-165-13
12	1135.5	63.0	328	4	US-07-791-931-7
13	1129	63.0	318	1	US-07-704-288C-9
14	1129	63.0	318	1	US-08-379-259-9
15	1126	62.8	328	4	US-07-791-931-5
16	1120	62.5	330	1	US-07-704-288C-8
17	1120	62.5	330	1	US-08-379-259-8
18	1108.5	61.9	314	1	US-07-704-288C-7
19	1108.5	61.9	314	1	US-08-379-259-7
20	1077.5	60.1	302	2	US-08-475-427-6
21	1077.5	60.1	302	2	US-07-842-165-6
22	1055	58.9	266	4	US-08-812-025-10
23	1055	58.9	266	4	US-07-791-931-10
24	1055	58.9	266	4	US-09-138-873A-10
25	986.5	55.1	254	2	US-08-475-427-1
26	986.5	55.1	254	2	US-07-842-165-1
27	986.5	55.1	254	4	US-08-448-398-3

Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 37, Appli
Sequence 35, Appli
Sequence 36, Appli
Sequence 10, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 8, Appli
Patent No. 5187262
Sequence 14, Appli

28 818.5 45.7 254 1 US-08-047-413-9
29 818.5 45.7 254 3 US-08-229-050-9
30 818.5 45.7 254 3 US-08-801-563-9
31 809 45.1 253 1 US-08-162-475A-5
32 784 43.8 253 4 US-07-791-931-9
33 781.5 43.6 253 1 US-08-162-475A-2
34 779.5 43.5 250 1 US-08-162-475A-4
35 765 42.7 316 4 US-07-791-931-8
36 707.5 39.5 372 4 US-07-791-931-4
37 512 28.6 130 3 US-08-329-799-37
38 437 24.4 148 3 US-08-329-799-35
39 232 12.9 51 3 US-08-329-799-36
40 213 11.9 211 2 US-08-935-886-10
41 212 11.8 71 1 US-07-704-288C-15
42 212 11.8 71 1 US-08-379-259-15
43 212 11.8 208 2 US-08-935-886-8
44 200.5 11.2 209 6 5187262-2
45 198 11.0 63 1 US-07-704-288C-14

ALIGNMENTS

RESULT 1
US-07-704-288C-3
; Sequence 3, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-704-288C-3

Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 1.6e-103;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

4 LRARCATAVLAVLVAAVLPATAEQCSQAGKACDLCSCQFGCGTSDYCGPRCQ 63
1 MRALAVVAVAREFLAAV---HAECGSGAGGAVCPNCLCCSQFGCGTSDYCGAGCQ 57

Pive

us-09-534-229c-2.ra1

Tue May 7 10:52:16 2002

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QY 64 SQCT-----CGGGGGGVSIVSRDLFRFLHNRNDAACLRARFYTYDAFLAAGAF 115
Db 58 SQSRLRRRPPDASGGGGGVSIVSRSLFDMLLHNRNDAACFPASNFYTYDAFVAASAF 117
QY 116 PARCTTGDLTRKREVAARFGQSHETTGWPTAPDGPFGSWGCFKQEQ-GSPPSYCDQS 174
Db 118 PGFAAGADADTNKREVAARFLAQSHETTGWATAPDGPYTWGCFKRENGGAGDPDYCQS 177
QY 175 ADWPCAPKQYGRGPQLTHNINYPAGRAIGVDDLNNPDLVATDPTVAFKTAIWFWMT 234
Db 178 AQWPCAAKYYGRGPQLSINYNYPAGQAIGADLLGDPDLVASDATVSFDTAFNFWMT 237
QY 235 TQSNKPSCHDVITGLWPTARDSAAGRVPGYVTINNGIEGCMQNDKVADRIGFYK 294
Db 238 PQSPKPCNAVATQWTPSADQAGRVPYGVITININGLECGHGGEDDRIADRIGFYK 297
QY 295 RYCDIFGIGYGNLDCYNQ 313
Db 298 RYCDILGVSYGANLDCYSQ 316

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RESULT 2
US-08-093-372-2
; Sequence 2, Application US/08093372
; Patent No. 5530187
; GENERAL INFORMATION:
; APPLICANT: Lamb, Christopher J.
; APPLICANT: Zhu, Qun
; APPLICANT: Maher, Bileen A.
; APPLICANT: Dixon, Richard A.
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
; TITLE OF INVENTION: DISEASE RESISTANCE GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,372
; FILING DATE: 16-JUL-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9391
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-093-372-2

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Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 1.6e-103;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

QY 4 LRARCATAVLAIVLAARVTPATNEQCSQAGGAKACDLCCSQFGCGTTSYDYCGPRQC 63
Db 1 MRALAVVAVVAVRPFLLAAAV---HAEQCSQAGGAVCPNCLCCSQFGWCGSTSDYCGAGCQ 57

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QY 64 SQCT-----CGGGGGGVSIVSRDLFRFLHNRNDAACLRARFYTYDAFLAAGAF 115
Db 58 SQSRLRRRPPDASGGGGGVSIVSRSLFDMLLHNRNDAACFPASNFYTYDAFVAASAF 117
QY 116 PARCTTGDLTRKREVAARFGQSHETTGWPTAPDGPFGSWGCFKQEQ-GSPPSYCDQS 174
Db 118 PGFAAGADADTNKREVAARFLAQSHETTGWATAPDGPYTWGCFKRENGGAGDPDYCQS 177
QY 175 ADWPCAPKQYGRGPQLTHNINYPAGRAIGVDDLNNPDLVATDPTVAFKTAIWFWMT 234
Db 178 AQWPCAAKYYGRGPQLSINYNYPAGQAIGADLLGDPDLVASDATVSFDTAFNFWMT 237
QY 235 TQSNKPSCHDVITGLWPTARDSAAGRVPGYVTINNGIEGCMQNDKVADRIGFYK 294
Db 238 PQSPKPCNAVATQWTPSADQAGRVPYGVITININGLECGHGGEDDRIADRIGFYK 297
QY 295 RYCDIFGIGYGNLDCYNQ 313
Db 298 RYCDILGVSYGANLDCYSQ 316

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RESULT 3
US-08-379-259-3
; Sequence 3, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-379-259-3

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```

Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 1.6e-103;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

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& at
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-047-413-11

Query Match          65.7%; Score 1177.5; DB 1;
Best Local Similarity 64.2%; Pred. No. 8.4e-99;
Matches 203; Conservative 45; Mismatches 65;

QY      8  CAVAVLAVVIAAAVTPATAEQCSQAGGAKCADCLCCSQFGFC
Db      4  CKFTALSLFLSLLLSASAEQCSQAGGARCAGSLCCSKFGW
QY      67  TG- -CGSGGGGVASIVSRDLPERFLLRHNDAACLARGFTYDAFLAAAGAFPAFGITGL 124
Db      64  PGGTTPGGGDLGSLIISSMFDQMLKHNDAACQCGKGFYSNAFINAARSPFGTSGDT 123
QY      125  DTRKREVAARFGQTSHETTGWPTAPDGFPSVGYCFKQEQSPSPYCDQADWPACPKQ 184
Db      124  TARKEIAAFAAQTSHETTGWATAPDGPYAWGYCWLREQCSFGDYCTPSGOWPCAPGKH 183
QY      195  YVGRGPIQLTHNYNGPAGRAIGVDLLNNPDVAVDPTVAFTATLFWMTTOSNKPSCHD 244
Db      184  YVGRGPIQLSHNYNGPGRALGVDLLNNPDVAVDPTVIFSALFWMTTOSNKPSCHD 243
QY      245  VITGLWTPPTARDAAGRVPYGVITWNINGGIECGMGQNDKVADRIFGFYKRYCDIFGIY 304
Db      244  VIIGRQPSADEANRLPFGVITNIINGLEGCGRTDSRVQDRIGFYRKYCSILGVSP 303
QY      305  GNNLDCYNOLSNVGL 320
Db      304  GNNLDCGNQRSFNGL 319

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RESULT 5
US-08-229-050-11
; Sequence 11, Application US/08229050
; Patent No. 6065491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vioemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-229-050-11

Query Match 65.7%; Score 1177.5; DB 3; Length 324;
Best Local Similarity 64.2%; Pred. No. 8.4e-99;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;

QY 8 CATAVLAVLAAAVTATACQCGAGGACADCLCCSQFGCGTTSYDYGCP-RCQSQC 66
Db 4 CKFTALSSLLSLLSASAEQCGAGGACASGLCCSKFGWCGNTNDYCGPGNCQSQC 63
QY 67 TG--CGGGGGGVASIVSRDLFERLLHRNDAACLARGFYTYDAFLAAAGAPPAGFTTGD 124
Db 64 PGGPTPPGGGLGSISSMDFDMLKHNDAACQKGFYSYNAFTNAARSPFGFTSGDT 123
QY 125 DTRKREVAFFQGTSHETTGWPAPDGPFSWGYCFKQEQSPSYCDQSDADWPCAPGKQ 184
Db 124 TARKEIAAFAAQTSHETTGWATPDGPYAWGYCWLREQCSPGDYCTPSGOWPCAPGRK 183
QY 185 YVGRPIQLTHNYGPGRAIGVDLLNPNLDVADPTVAEKTALFWMTTQSNKPSCHD 244
Db 184 YFGRGPIQISHNYGPGRAIGVDLLNPNLDVADPTVIFSKALFWMTTQSPKPSCHD 243
QY 245 VITGLWTPATDAAAGRVPGYGVITNVINGIECGMGQNDKVADRIKFYKRYCDIFGIGY 304
Db 244 VIIGRWQPSADRAANRLPGFVITNIINGLECGRGTDTSRVQDRIGFYRYRYSILGVSP 303
QY 305 GNNLDCYNQLSFNVGL 320
Db 304 GDNLDGNGQSRFNGNL 319

RESULT 7
US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikbel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
;

; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-229-050-11

Query Match 65.7%; Score 1177.5; DB 3; Length 324;
Best Local Similarity 64.2%; Pred. No. 8.4e-99;
Matches 203; Conservative 45; Mismatches 65; Indels 3; Gaps 2;

QY 8 CATAVLAVLAAAVTATACQCGAGGACADCLCCSQFGCGTTSYDYGCP-RCQSQC 66
Db 4 CKFTALSSLLSLLSASAEQCGAGGACASGLCCSKFGWCGNTNDYCGPGNCQSQC 63
QY 67 TG--CGGGGGGVASIVSRDLFERLLHRNDAACLARGFYTYDAFLAAAGAPPAGFTTGD 124
Db 64 PGGPTPPGGGLGSISSMDFDMLKHNDAACQKGFYSYNAFTNAARSPFGFTSGDT 123
QY 125 DTRKREVAFFQGTSHETTGWPAPDGPFSWGYCFKQEQSPSYCDQSDADWPCAPGKQ 184
Db 124 TARKEIAAFAAQTSHETTGWATPDGPYAWGYCWLREQCSPGDYCTPSGOWPCAPGRK 183
QY 185 YVGRPIQLTHNYGPGRAIGVDLLNPNLDVADPTVAEKTALFWMTTQSNKPSCHD 244
Db 184 YFGRGPIQISHNYGPGRAIGVDLLNPNLDVADPTVIFSKALFWMTTQSPKPSCHD 243
QY 245 VITGLWTPATDAAAGRVPGYGVITNVINGIECGMGQNDKVADRIKFYKRYCDIFGIGY 304
Db 244 VIIGRWQPSADRAANRLPGFVITNIINGLECGRGTDTSRVQDRIGFYRYRYSILGVSP 303
QY 305 GNNLDCYNQLSFNVGL 320
Db 304 GDNLDGNGQSRFNGNL 319

RESULT 6
US-08-801-563-11
; Sequence 11, Application US/08801563
; Patent No. 6087560
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Seia-Buurlage, Marianne B.
; APPLICANT: Vloeemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
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US-07-791-931-6
Query Match      65.7%; Score 1176.5; DB 4; Length 310;
Best Local Similarity 67.2%; Pred. No. 9.8e-99;
Matches 201; Conservative 41; Mismatches 54; Indels 3; Gaps 2;

QY 25 ATAECGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSQCTG--CGGGGGGVASIVS 81
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 ASAEQCGSAGAGACACDLCCSGFGCGTTSYDYGCP-RCQSQCTG--CGGGGGGVASIVS 66
QY 82 RDLFERELLHRNDAAACLAGFYTYDAFLAAGAFPAFTGDTLTKRREVAFAFFQTSHE 141
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 SSMFDQMLKLRNDNACQKGYFYNAFNAARSPFGFTSGDTTARKREIAAFAFFQTSHE 126
QY 142 TTGGWPTAPDGFSGYCFKQBGQSPSYCQDSADWPCAPKQYGRGPIQLTHNYNYP 201
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 TTGGWATAPDGFYANGYCWLRQGSFGDYCTPSGQWPCAPGKRYGFGPIQISHNYNYP 186
QY 202 AGRATGVLLNPNLDVATDPTVAFKTAIWFMWMTQSNKPSCHDVITGLWTPARDASAAGR 261
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 CGRATGVLLNPNLDVATDPTVAFKTAIWFMWMTQSNKPSCHDVITGLWTPARDASAAGR 246
QY 262 VPGYGVITNINNGLECGRGTDVSRVQDRIGFYKRYCDIFGICYGNLDCYNQLSFNVGL 320
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 LPFGFVITNINNGLECGRGTDVSRVQDRIGFYKRYCDIFGICYGNLDCYNQLSFNVGL 305

RESULT 8
US-07-704-288C-6
; Sequence 6, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-704-288C-6

US-07-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-6

Best Local Similarity 67.2%; Pred. No. 7.1e-98;
Matches 201; Conservative 41; Mismatches 53; Indels 4; Gaps 3;

QY 25 ATAECGSGAGACACDLCCSGFGCGTTSYDYGCP-RCQSQCTG--CGGGGGGVASIVS 81
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 ASAEQCGSAGAGACACDLCCSGFGCGTTSYDYGCP-RCQSQCTG--CGGGGGGVASIVS 67
QY 82 RDLFERELLHRNDAAACLAGFYTYDAFLAAGAFPAFTGDTLTKRREVAFAFFQTSHE 141
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 SSMFDQMLKLRNDNACQKGYFYNAFNAARSPFGFTSGDTTARKREIAAFAFFQTSHE 127
QY 142 TTGGWPTAPDGFSGYCFKQBGQSPSYCQDSADWPCAPKQYGRGPIQLTHNYNYP 201
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 128 TTGGWATAPDGFYANGYCWLRQGSFGDYCTPSGQWPCAPGKRYGFGPIQISHNYNYP 187
QY 202 AGRATGVLLNPNLDVATDPTVAFKTAIWFMWMTQSNKPSCHDVITGLWTPARDASAAGR 261
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 188 CGRATGVLLNPNLDVATDPTVAFKTAIWFMWMTQSNKPSCHDVITGLWTPARDASAAGR 246
QY 262 VPGYGVITNINNGLECGRGTDVSRVQDRIGFYKRYCDIFGICYGNLDCYNQLSFNVGL 320
D  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 LPFGFVITNINNGLECGRGTDVSRVQDRIGFYKRYCDIFGICYGNLDCYNQLSFNVGL 305

RESULT 9
US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; DEFENSE REGULATORY
; ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-6

Query Match      65.1%; Score 1167; DB 1; Length 310;

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Best Local Similarity 67.2%; Pred. No. 7.le-98;
Matches 201; Conservative 41; Mismatches 53; Indels 4; Gaps 3;

QY 25 ATAEOGSGAGCAKADICCSQFCCGTTSYCGP-RCSQCTG--CGGGGGGVASIVS 81
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 8 ASAEQGSQAGGARCASGLCCSKFGWGNNDYDGFNGNCSQCPCGPPTPPGGDLGSIIS 67
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
QY 82 ROLFPERFLHRNDAACLAGFYTYDAFLAAGAFAFGTTIGDLDFRKPEVAAFGOTSHE 141
::| | ||||| :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 68 SSMFDQLMRHNDNACQGKFYSYNAFINAAKSFFGFTSTTKRREIAAFFAQTSHE 127
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
QY 142 TTGGWTATPDGPFPSWCYCFKQOQSGPPSYCDQSADWPAPGRKYXRGPIQLTHNYNYP 201
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 128 TTGGWTATPDGPYAWGYCWLREGSGEGDYCTFSQWPCAPGRKYFGRGPIQISHYNYGP 187
|:|||||||:~| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
QY 202 AGRAIGVDLLNNPDVLVATDPTVAKTAINFWMTTOSNKPSCHDVITGLWTPARDSAAGR 261
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 188 CGRAIGVDLLNNPDVLVATDPVISFKALSALWFMTPOSPKPSCHDVITIGRW-PSSADRAANR 246
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
QY 262 VPGYGVTNVINGIEGCGQNDKVADRIGFYKRYKIDFCIGYGNLDCYNOLSENUGL 320
|:|||||||:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
DB 247 LPFGVITNLINGLECGRGTRDSRVQDRIGFYRRYCILGVSPGDNLDCGNRSFGNGL 305
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RESULT 10
US-08-475-427-13
; Sequence 13, Application US/08475427
; Patent No. 5859340
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: PIGNARD, Annie
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,427
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,165
; FILING DATE: 01-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00607
; FILING DATE: 21-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90 09460
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/564/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; LENGTH: 329 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-842-165-13

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Query Match	63.7%;	Score 1141.5;	DB 2;	Length 329;
Best Local Similarity	59.9%;	Pred. NO. 1.5e-95;		
Matches 104.	Conservative	54.	Mismatches 69;	Indels 7;
				Gaps 3;

[illegible]

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RESULT 12
US-07-791-931-7
; Sequence 7, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Phaseolus vulgaris
US-07-791-931-7

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Query Match	63.4%;	Score 1135.5;	DB 4;	Length 328;
Best Local Similarity	63.6%;	Pred. No. 5.3e-95;		
Matches 106;	Conservative	44.	Mismatches 67.	Indels 1;
	Gaps			1;

[illegible]

Db	192	ISWNYGQCGRALGVDDLLKPLD	VATDSV	ISFKSALWFMTAQSPKPS	SSHDI	VITSRWP	255
QY	253	TARDSAARGVPYGV	VTNVINGIECGMGONDKVAD	RIGFYKRYCDIFGIGYGN	NDLDCYN	312	
Db	252	SSADVAARRUPPGV	VTNIIINGLECGRGQDSR	VDRIFFKRYCDLLGVGYGN	LDLDCYS	311	
QY	313	QLSFNVGL	320				
Db	312	QTDFGNSL	319				

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Query Match	63.0%;	Score 1129;	DB 1;	Length 318;
Best Local Similarity	63.6%;	Pred. No. 2e-94;		
Matches 196;	Conservative	42;	Mismatches 68;	Indels 2;
				Gaps 1;

[illegible]

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Db      182 ISWNTNYQCGRAGVLDLLNKPDVLVA2DSVFKSALWFWMWTASQPKSPSHDVITSKWP 241
QY      253 TARDAAAGRPVGYGVITNVINGTECGMGQNDKVADRIGFYKRKYCDLFGIGYGNNLDYCN 312
Db      242 SADVAARLRPGYGVITNVINGLECGRGDSRVQDRDIGRFKRYCDDLGGVYGNLDCYS 301
QY      313 QLSFNNVGL 320
Db      302 QTFFGNSL 309

RESULT 14
US-08-379-259-9
; Sequence 9, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-9

Query Match          63.0%; Score 1129; DB 1; Length 318;
Best Local Similarity 63.6%; pred. No. 2e-94;
Matches 196; Conservative 42; Mismatches 68; Indels 2; Gaps

QY      13 LAVVILAAAVPTATRAEQCSAGGAKACDCLCCSQCFEGCTTSDYCGPRCQSQCCTGGGG 72
Db      4 VGVVMALLLVGSYGCGRQAGGALCPGGNCCSQFGWCSTTDYCYGPGCQSQCGPSPA 63
QY      73 GGVVASIVSRDLFERFLHRNDACLARGFTYDAFLAAGAFAFPAGTTGDLDTRKEVA 132
Db      64 PTDSLALSIRSFDFQMLRHNDGACPAGKGFYTYDAFLAATAKAYFSFNIGDTAFRKREIA 133
QY      133 AFFGTGTSHTTGWPTAPDGPFWSGVCYFKQPCQSPPSYCQDSADWPCAPKQYVGPIQ 192

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1330	74.2	339	2	S39979	chitinase (EC 3.2.2.13)
2	1326.5	74.0	340	2	S40414	chitinase (EC 3.2.2.13)
3	1315	73.4	302	2	JC2071	chitinase (EC 3.2.2.13)
4	1297	72.4	318	2	T04403	probable chitinase
5	1287.5	71.8	332	2	T04484	probable chitinase
6	1283	71.6	320	2	S38670	chitinase (EC 3.2.2.13)
7	1272	71.0	335	2	T03239	probable chitinase
8	1238.5	69.1	323	2	T03614	chitinase (EC 3.2.2.13)
9	1230	68.6	336	2	SI5997	chitinase (EC 3.2.2.13)
10	1218	68.0	318	2	SI4948	chitinase (EC 3.2.2.13)
11	1196.5	66.8	324	2	S56694	chitinase (EC 3.2.2.13)
12	1193	66.6	318	2	S65019	chitinase (EC 3.2.2.13)
13	1192	66.5	322	2	S54016	chitinase (EC 3.2.2.13)
14	1187.5	66.3	311	2	T07838	chitinase (EC 3.2.2.13)
15	1185	66.1	332	1	S37344	chitinase (EC 3.2.2.13)
16	1184	66.1	324	2	S20981	chitinase (EC 3.2.2.13)
17	1181	65.9	329	2	S08627	chitinase (EC 3.2.2.13)
18	1177	65.7	318	2	S43317	chitinase (EC 3.2.2.13)
19	1174	65.5	316	2	S65020	chitinase (EC 3.2.2.13)
20	1173.5	65.5	319	2	JC2252	chitinase (EC 3.2.2.13)
21	1168	65.2	327	2	T09687	chitinase (EC 3.2.2.13)
22	1163	64.9	324	2	T10802	chitinase (EC 3.2.2.13)
23	1154	64.4	335	2	B45511	chitinase (EC 3.2.2.13)
24	1149.5	64.1	321	2	S57482	chitinase class 1
25	1146	64.0	322	2	S59953	chitinase (EC 3.2.2.13)
26	1145.5	63.9	320	2	S29947	chitinase (EC 3.2.2.13)
27	1144.5	63.9	334	2	S20982	chitinase (EC 3.2.2.13)
28	1143	63.8	332	2	T10810	chitinase (EC 3.2.2.13)
29	1130.5	63.1	327	1	JQ0365	chitinase (EC 3.2.2.13)

chitinase (EC 3.2.1.14) - rice
 C:Species: Oryza sativa (rice)
 C>Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S40414
 R:Nishizawa, Y.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S40414
 A:Accession: S40414
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-340 <NIS>
 A:Cross-references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:33-74/Domain: hevein chitin-binding domain homology <HCB>
 F:92-330/Domain: plant chitinase homology <PCH>

Query Match 74.0%; Score 1326.5; DB 2; Length 340;
 Best Local Similarity 70.9%; Pred. No. 2.6e-94;
 Matches 241; Conservative 29; Mismatches 53; Indels 17; Gaps 3;

Qy 1 MSTLRARCATA-----VLAVLAAAVTPATAEQGSGAGKACADCLCCSQFPGCTTS 55
 Db 1 MSTPRAASTAKKAAALVALAALATAARAEQGAAGARCPNCLCCSRWGCPTTS 60
 Qy 56 DYCPGRCQCTGCG-----GGGGVAVSRDLPERLLHRNDAACLAGFYTYDA 107
 Db 61 DFCGDCGSCSGCGPTPTPPSPDSGVSIVPRDLPERLLHRNDGACPARFYTYEA 120
 Qy 108 FLAAGAFPAGTGGDLDTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEGSP 167
 Db 121 FLAAAAAPAPFGTGTETRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEQNP 180
 Qy 168 PSYCDQSDWPCAPGKQYGRPIQLTHNYNGPAGRAIGVDLLNPDVATDTPVAFKT 227
 Db 191 SDYQSPFPCAPGKRYGRPIQLSFNFNYPAGRAIGVDLLNPDVATDTPVAFKT 240
 Qy 228 ALFWMTTQSNKPSCHDVITGLWPTARDSAAGRPYGVITNVINGIEGGMGNDKVA 287
 Db 241 ALFWMTTQGNKPSCHDVITGRWAPSPADAAAGRAPYGVITNVINGIEGGMGNDKVA 300
 Qy 288 DRIGFYKRYCDIFGIGYNNLDYNNLSFN----VGLAAQ 323
 Db 301 NRIGFYQRYCAFAGTGTGNNLDYNNLCPNFNSGVGLAEQ 340

RESULT 3
 JC2071
 chitinase (EC 3.2.1.14) a - rye
 C:Species: Secale cereale (rye)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
 C:Accession: JC2071
 R:Yamagami, T.; Funatsu, G.
 Biosci. Biotechnol. Biochem. 58, 322-329, 1994
 A:Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale
 A:Reference number: JC2071; MUID:94169514
 A:Accession: JC2071
 A:Molecule type: protein
 A:Residues: 1-302 <YAM>
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-42/Domain: hevein chitin-binding domain homology <HCB>
 F:64-302/Domain: plant chitinase homology <PCH>

Query Match 73.4%; Score 1315; DB 2; Length 302;
 Best Local Similarity 76.1%; Pred. No. 3.8e-93;
 Matches 229; Conservative 24; Mismatches 36; Indels 12; Gaps 1;

Qy 28 EQCGSAGGACADCLCCSQFPGCTTSYCGPRGSCQCTGCG-----GGGG 75
 Db 1 EQCGSAGGATCPNCLCCSRFGWCGSTSYCGDCCSQACGCGGGTPTPTPTPSGGG 60

Qy 76 VASIVSRDLPERLLHRNDAACLAGFYTYDAFLAAAGAPFAFGTGGDLDTRKREVAFF 135
 Db 61 VSSIVSRALFDRMLLRNDGACQAKGFYTYDAFVAAAGAPFGTGGTSTDRKREVAFL 120
 Qy 136 GQTSHTTGGWPTAPDGPFSWGYCFKQEGSPSYCDQSDWPCAPGKQYGRPIQLTH 195
 Db 121 AQTSHTTGGWATPDGAFAGWGYCFKQERGATSNICYTPSAQWPCAPGKSYGRPIQLSH 180
 Qy 196 NNYGYPAGRAIGVDLLNPDVATDTPVAFKTAIFWMTTQSNKPSCHDVITGLWPTAR 255
 Db 181 NNYGYPAGRAIGVDLLNPDVATDTPVSKTAMFWMTAQAPKPSHAVITGOWSPSGT 240
 Qy 256 DSAAGRPYGVITNVINGIEGGMGNDKVADRIGFYKRYCDIFGIGYNNLDYNNLS 315
 Db 241 DRAAGRPYGVITNVINGIEGGMGNDKSRVADRIGFYKRYCDILGVGYNLDYNNQRP 300
 Qy 316 F 316
 Db 301 F 301

RESULT 4
 T04403
 probable chitinase (EC 3.2.1.14) precursor - barley
 C:Species: Hordeum vulgare (barley)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
 C:Accession: T04403
 R:Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
 submitted to the EMBL Data Library, September 1993
 A:Description: Isolation and characterization of a barley chitinase genomic clone.
 A:Reference number: Z15336
 A:Accession: T04403
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-318 <IGN>
 A:Cross-references: EMBL:U02287; NID:g495304; PIDN:AAAL8586.1; PID:g495305
 A:Experimental source: cv. NK1558
 C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-318/Product: chitinase #status predicted <MAT>
 F:20-60/Domain: hevein chitin-binding domain homology <HCB>
 F:80-318/Domain: plant chitinase homology <PCH>

Query Match 72.4%; Score 1297; DB 2; Length 318;
 Best Local Similarity 74.0%; Pred. No. 4.4e-92;
 Matches 233; Conservative 27; Mismatches 43; Indels 12; Gaps 3;

Qy 12 VLAVLAAAVTPATAEQGSGAGKACADCLCCSQFPGCTTSYCGPRGSCQCTGCG 71
 Db 5 VLFVAVMAA--TMAVEQCGSQAGGATCPNCLCCSRFGWCGST--PYCGDGGCQSCSGCG 62
 Qy 72 -----GGGVASIVSRDLPERLLHRNDAACLAGFYTYDAFLAAAGAPFAFGT 121
 Db 63 GSTPTPTPSGGGVSSIVSRALFDRMLLRNDGACQAKGFYTYDAFVAAASAFRGFTT 122
 Qy 122 GLDTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCFKQEGSPSYCDQSDWPCAP 181
 Db 123 GGTDRKREVAAPFAQTSHETTGGWATPDGAFAGWGYCFKQERGATSNICYTPSAQWPCAP 182
 Qy 182 GKQYGRPIQLTHNYNGPAGRAIGVDLLNPDVATDTPVAFKTAIFWMTTQSNKPS 241
 Db 183 GKSYGRPIQLSHNYNGPAGRAIGVDLLNPDVATDTPVAFKTAIFWMTAQAPKPS 242
 Qy 242 CHDVITGLWPTARDSAAGRPYGVITNVINGIEGGMGNDKVADRIGFYKRYCDIFG 301
 Db 243 SHAVITGOWSPSGTDRAGRPVFGVITNVINGIEGGMGNDKSRVADRIGFYKRYCDILG 302
 Qy 302 IGYNNLDYNNLSF 316
 Db 303 VGYNNLDYNSQRPF 317

```
RESULT 5
T04484
C:probable chitinase (EC 3.2.1.14) - barley
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T04484
R:Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A:Title: Identification of an enhancer/silencer sequence directing the aleurone-specific
A:Reference number: Z15373; MUID:95078949
A:Accession: T04484
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-332 <LEA>
A:Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961
C:Genetics:
A:Gene: CH133
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:28-69/Domain: hevein chitin-binding domain homology <HCB>
F:85-322/Domain: plant chitinase homology <PCH>

Query Match 71.8%; Score 1287.5; DB 2; Length 332;
Best Local Similarity 71.0%; Pred. No. 2.4e-91;
Matches 230; Conservative 35; Mismatches 44; Indels 15; Gaps 4;

QY 11 AVLAIVLAAAVTP--ATAECGSGAQGAKCADCLCCSGFCGCTTSDYCGPCGSOCTG 68
DB 9 AIVAIVLSAALAMWYRAOCCGSGAQGATCPNCLCCSKFSGCTSDYCGAGCQSCG 68
QY 69 CG-----GGGGVASIVSRDLFRFLHNRN--DAACLAGFTYDAFLAAAGAFPAFG 119
DB 69 CGPTPPGSPGGVSSILSRDLFQFLHNRDQDA--GFTYDAFLAAATFPFAG 124
QY 120 TGDLDTRKREVAFFGCTSHETTGWPTAPDGFPSWGYCFKQCGSPSYCDQSDAWPC 179
DB 125 TTGSTETRKQVAAFFGCTSHETTGWATAPDGPYSWGYCYRRELGSPPDYCPSSOWPC 184
QY 180 APGYGYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNK 239
DB 185 VQDQYGYRGFIMLSWNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNK 244
QY 240 PSCHVITGLWPTARSDAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDI 299
DB 245 PSSHAVITGWTPTAADTAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCNI 304
QY 300 FGIYGNLDCYINQLSPNVLAAQ 323
DB 305 LGVGYGNLDCYNQRPVEGLLIQ 328

RESULT 6
S38670
Chitinase (EC 3.2.1.14) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
C:Accession: S38670
R:Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener, H.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38670
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <LIA>
A:Cross-references: EMBL:X76041; NID:q416028; PIDN:CAA53626.1; PID:q416029
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-320/Domain: plant chitinase homology <PCH>
```

```
Query Match 71.6%; Score 1283; DB 2; Length 320;
Best Local Similarity 70.5%; Pred. No. 5.2e-91;
Matches 222; Conservative 34; Mismatches 49; Indels 10; Gaps 1;

QY 12 VLAVLAAAVTATATACGSGAQGAKCADCLCCSGFCGCTTSDYCGPCGSOCTGCGG 71
DB 5 VVAMLAFAFAVSAHAPECGSQAGGATCPNCLCCSKFSGCTSDYCGNGCQSCGCG 64
QY 72 G-----GGGVASIVSRDLFRFLHNRNDAACLAGFTYTYDAFLAAAGAFPAFGTT 121
DB 65 GGPVPVPTFTGGVSSIIQSLEFDQMLLHNRDAACQAKGFYNGAFVAAANSFGEATT 124
QY 122 GDLDRKREVAFFGCTSHETTGWPTAPDGFPSWGYCFKQCGSPSYCDQSDAWPCAP 181
DB 125 GGADVRKREVAFFGCTSHETTGWPTAPDGPYSWGYCFKQCGSPSYCDQSDAWPCAP 184
QY 182 GKQYGYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNKPS 241
DB 185 GKRYFGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAIWFWMTQSNKPS 244
QY 242 CHDVITGLWPTARSDAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIFG 301
DB 245 SHDVITGRWSPSGADQAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDILG 304
QY 302 IGYGNLDCYNQLSF 316
DB 305 VTYGNLDCYNQRPF 319

RESULT 7
T03239
probable chitinase (EC 3.2.1.14) precursor - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
C:Accession: T03239
R:Anuratha, C.S.; Mew, T.; Muthukrishnan, S.
submitted to the EMBL Data Library, September 1993
A:Description: Induction of chitinases and beta-glucanases in Rhizoctonia solani infe
A:Reference number: Z14854
A:Accession: T03239
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-335 <ANU>
A:Cross-references: EMBL:U02286; NID:q495302; PIDN:AAA18585.1; PID:q495303
A:Experimental source: leaf, strain IR58
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-335/Product: chitinase #status predicted <MAT>
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:90-325/Domain: plant chitinase homology <PCH>
```

```
Query Match 71.0%; Score 1272; DB 2; Length 335;
Best Local Similarity 70.1%; Pred. No. 3.8e-90;
Matches 237; Conservative 27; Mismatches 56; Indels 18; Gaps 6;

QY 1 MSTLRARCATA-----VLAVLAAAVTATATACGSGAQGAKCADCLCCSGFCGCTTS 55
DB 1 MSTPRAASLAKKAALVALAVLAAALATAACAEQCGAGGAGCARPCNCLCCSRWGCSTS 60
QY 56 DYCGPCGSOCTGCG-----GGGGVASIVSRDLFRFLHNRNDAACLAGFTYTYDAFL 109
DB 61 DFCGDCGSOCSGCGTPTTPPSPSGVGSIVPRDLFRFLHNRNDAACLAGFTYTYDAFL 120
QY 110 AAGAFPAFGTTGDTDRKREVAFFGCTSHETTGWPTAPDGFPSWGYCFKQCGSPPS 169
DB 121 RRA-APPAPGGTDETRKREVAFFGCTSHETTGWPTAPDGFPSWGYCFKQCGSPPS 179
QY 170 QCDQSDAWPCAPGKYGRGPIQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAFTAI 229
DB 180 YCQPFAGWPCAPGRKYGRGPIQLSFNFNGPAGRAIGVDLLSNPDLVATDPTVAFTAI 239
```

QY 230 WFWMTQSNKPSCHDVITGLWTFPTARDSSAAGRVPGYGVIINVLINGIECGMGQNDKVADR 289
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 240 WFWMTPOGKNPSSHVDVITGWAP--RREVAAGRA-GYGVITIIVNGGLECGDGPDDRVRN 297

QY 290 IGFVKRYCDIFGTGYGNLDCYNQLSFN----VCLAAQ 323
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 298 IGFYQAYCGAFGI GTGNLDCYNQRPNFNSGSYGLAEQ 335

RESULT 8
T03614
chitinase (EC 3.2.1.14) - rice
N/Alternate names: endochitinase
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C/Accession: T03614
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A>Title: Sequence variation, differential expression and chromosomal location of rice chitinase
A/Reference number: S39979; MUID:94049667
A/Accession: T03614
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-323 <NIS>
A/Cross-references: EMBL:D16221; NID:g452232; PIDN:BAA03749.1; PID:g500615
A/Experimental source: cv. Nipponbare
C/Genetics:
A/Gene: Cit-1
C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C/Keywords: glycosidase; hydrolase
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-322/Domain: plant chitinase homology <PCH>

Query Match 69.1%; Score 1238.5; DB 2; Length 323;
Best Local Similarity 69.3%; Pred. No. 1.3e-87;
Matches 224; Conservative 31; Mismatches 51; Indels 17; Gaps 4;

QY 9 ATAVLVVLAATAVPATACGGSQAGAKCADLCSCQFGCGTTSDYCGPRCQSCTG 68
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 3 ALAVV-VVATAFAVVAVRGEGCGSAGALCPNLCCSQYGCWGSGTSAYCGSQCSQG 61

QY 69 -----CGGGGGVGASIVSRDLERFLIHENDAACLAGFYTYDAFLAAGAPPF 118
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 62 SCGGGGTPPSGGGGVGASIVSRSLFDQMLLRNDAAACPAKFYYTYDAFVAANAPPF 121

QY 119 GTTGDLTRKEVAFFGQTSHETGGWAPTADGPFPSWGYCFKOEQ---GSPPSYCDQS 174
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 122 ATTGDAATRKEVAFAAQAOTSHEITGGWATPADGPGYSWGYCFKEENNGNVGS--DYCVQS 179

QY 175 ADWPCAPKQYGRGPQLTHNYNYGPAIGAIGVLDILNNPDLYATDTVAFKTAIWFMT 234
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 180 SQWPCAAGKKYGRGPQISINYNYGPAIGASVLLNSLPDLVASDAIVSKTAIWFMT 239

QY 235 TQSNKPSCHDVITGLWTFPTARDSAAGRVPGYGVIINVLINGIECGMGQNDKVADRIGFYK 294
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 240 PQSPKPSCHAWTQOWTPNGNQAGRVPYGVVTNIINGVEGCGHADSRVADRIGFYK 299

QY 295 RYCDFIGYGNLDCYNQLSFN 317
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 300 RYCDMLGVSYGANLDCYNQRPFN 322

RESULT 9
SI5997
chitinase (EC 3.2.1.14) - rice
C/Species: Oryza sativa (rice)
C/Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C/Accession: SI5997
R:Zhu, Q.; Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A>Title: Isolation and characterization of a rice gene encoding a basic chitinase.


```
QY 68 -----CCGGGGGASIVSRDLFERLLHRNDAACLAGFYTYDAFLAAGAFPAF 118
Db 62 QLRRRDRPSGGGGGASIVSRDLFERLLHRNDAACPAKMLTYDAFVAANAFPTF 121
QY 119 GTGGLDTRKREVAAFQGTSHETTGWTPADPGPSWGYCFKQEQ----GSPSPYCDQS 174
Db 122 ATTGDAIRKREVAAFQGTSHETTMGWATADPGPSWGYCFKREKNGNVGS--DYCVQS 179
QY 175 ADWPCAPKQYGRGPIQLTHNNYGPAGRAIGVDLLNPNPDLVATDPTVAFKTAIFWMT 234
Db 180 SQWPCFACRAGKYGRGPIQLTHNNYGPAGRAIGVDLLNPNPDLVATDPTVAFKTAIFWMT 238
QY 235 TQNKPSCHDVITGLWTPATDASAGRVPGYGVITNVINGIECGMGONDKVADRIGFYK 294
Db 239 PQSEKPSCHAVMTGQWTPNGNDQAAGRVPGYGVITNVINGIECGMGADSRVADRIGFYK 298
QY 295 RYCDIFGIGYGNLDCYNQLSFN 317
Db 299 RYCDMLGVSYGANLDCYNQRPFN 321
```

RESULT 14

T07838

chitinase (EC 3.2.1.14) - cucurbit

C;Species: Cucurbita sp. (cucurbit)

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000

C;Accession: T07838

R;Baka, M.

submitted to the EMBL Data Library, June 1998

A;Reference number: Z16165

A;Accession: T07838

A;Status: preliminary; translated from GB/EMBL/DDEJ

A;Molecule type: mRNA

A;Residues: 1-311 <S>A>

A;Cross-references: EMBL:AB015655; PIDN:PAA31131.1

C;Genetics:

A;Gene: chitp1

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;20-61/Domain: hevein chitin-binding domain homology <HCB>

F;75-311/Domain: plant chitinase homology <PCH>

```
Query Match 66.3%; Score 1187.5; DB 2; Length 311;
Best Local Similarity 69.0%; Pred. No. 1e-83;
Matches 211; Conservative 31; Mismatches 59; Indels 5; Gaps 2;
```

```
QY 15 VVLAATAVPATACQSGAGKACDCLCSQGFSGTTSYDYGCPRCQSQOC-----TCGG 70
Db 7 IVLAFVFLGAASQCGKQANGALCPNKLCCSQFGWCGNTDEYCKNNQCSQCTPFSTGGG 66
QY 71 GGGGASIVSRDLFERLLHRNDAACLAGFYTYDAFLAAGAFPAFGTGDLDTRKRE 130
Db 67 GGGGSGSIINEALYNQMLKSKDPCPSNGFYRYNAFITAAQSFSGFGTGTDAATKRE 126
QY 131 VAAFQGTSHETTGWTPADPGPSWGYCFKQEQGSPSPSYCDQADWPCAPKQYGRGP 190
Db 127 LAAFQGTSHETTGWATADPGYAWGYCFIRER--NQDVCYCPNQQWPCAAGQKYGRGP 185
QY 191 IQLTHNNYGPAGRAIGVDLLNPNPDLVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLW 250
Db 186 IQLTHNNYGPAGRALNUNLNPDLVATDPTVAFKTAIFWMTTQSNKPSCHDVITGRW 245
QY 251 TPTARDSAAGRVPGYGVITNVINGIECGMGONDKVADRIGFYKRYCDIFGIGYGNLDC 310
Db 246 QPSAADSAGRVPGYGVITNVINGIECGMGADSRVADRIGFYKRYCDLLGIGYGNLDC 305
QY 311 YNQLSF 316
Db 306 NNQRSF 311
```

RESULT 15

S37344

chitinase (EC 3.2.1.14) chi9 precursor - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: S37344; S38838; S25637

R;Danhash, N.; Wagenmakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.

Plant Mol. Biol. 22, 1017-1029, 1993

A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu

A;Reference number: S37341; MUID:94003061

A;Accession: S37344

A;Molecule type: mRNA

A;Residues: 1-322 <DAN>

A;Cross-references: EMBL:Z15140; NID:g19190; PIDN:CAA78845.1; PID:g19191

A;Accession: S38838

A;Molecule type: protein

A;Residues: 23-42;202-216;224-236;247-258 <DAN>

C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-322/Product: chitinase chi9 #status experimental <MAT>

F;23-65/Domain: hevein chitin-binding domain homology <HCB>

F;75-314/Domain: plant chitinase homology <PCH>

```
Query Match 66.1%; Score 1185; DB 1; Length 322;
Best Local Similarity 66.1%; Pred. No. 1.6e-83;
Matches 203; Conservative 41; Mismatches 61; Indels 2; Gaps 2;
```

```
QY 16 VLAATAVPATACQSGAGKACDCLCSQGFSGTTSYDYGCP-RCQSQCTGCGGGG 74
Db 11 LLFSVLLLSASAEQCGSAGGALCGLCCSKFGWCGNTNEICGPGNCQSCQCGGPGPSG 70
QY 75 GVASIVSRDLFERLLHRNDAACLAGR-GFYTYDAFLAAGAFPAFGTGDLDTRKREVA 133
Db 71 DLGGVINSMFQMLNHRNDNACQGNFYNAFVTAAGFPFGTGTDTAKREIAA 130
QY 134 FFGTSHETTGWTPADPGPSWGYCFKQEQGSPSPSYCDQADWPCAPKQYGRGPIQL 193
Db 131 FLAQTSHETTGWTPADPGYAWGYCFLEQGSFGDYCTPSSQWPCAPGRKYFGRGPIQI 190
QY 194 THNNYGPAGRAIGVDLLNPNPDLVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLWPT 253
Db 191 SHNNYGPAGRAIGVDLLNPNPDLVATDPTVAFKTAIFWMTTQSNKPSCHDVITGRWPS 250
QY 254 ARDSAAAGRVPGYGVITNVINGIECGMGONDKVADRIGFYKRYCDIFGIGYGNLDCYNQ 313
Db 251 GADQAANRVPGYGVITNVINGIECGHGSRSVQDRIGFYRRYCGILGVSPENLDCGNQ 310
QY 314 LSFNVL 320
Db 311 RSFGNGL 317
```

Search completed: May 3, 2002, 18:32:12

Job time: 7475 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:48:31 ; Search time 78.59 Seconds
(without alignments)
150.690 Million cell updates/sec

Title: US-09-534-229c-2

Perfect score: 1792

Sequence: 1 MSTLRARCATAVLAVLAAA.....YGNLDCYNQLSFNVGLAAQ 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1297	72.4	318	1	CH1L_HORVU
2	1230	68.6	336	1	CH12_ORYSA
3	1218	68.0	318	1	CH1L_ORYSA
4	1196.5	66.8	324	1	CH12_PEA
5	1193	66.6	318	1	CH1L_SOLTU
6	1185	66.1	322	1	CH1C_LYCES
7	1184	66.1	324	1	CH12_TOBAC
8	1181	65.9	329	1	CH1L_TOBAC
9	1177	65.7	318	1	CH13_SOLTU
10	1174	65.5	316	1	CH12_SOLTU
11	1166	65.1	321	1	CH1L_THECC
12	1163	64.9	324	1	CH1L_GOSHI
13	1154	64.4	322	1	CH1T_ARATH
14	1146	64.0	322	1	CH12_BRANA
15	1145.5	63.9	320	1	CH1X_PEA
16	1144.5	63.9	334	1	CH13_TOBAC
17	1143	63.8	302	1	CH12_GOSHI
18	1139	63.6	314	1	CH1B_VITVI
19	1135.5	63.4	328	1	CH1T_PHAVU
20	1130.5	63.1	327	1	CH15_PHAVU
21	1126	62.8	328	1	CH1T_SOLTU
22	1106	61.7	302	1	CH14_SOLTU
23	1055	58.9	266	1	CH12_HORVU
24	1010	56.4	340	1	CH16_POPTR
25	954	53.2	246	1	CH1D_LYCES
26	867	48.4	303	1	CH1B_POPTR
27	826.5	46.1	247	1	CH1B_LYCES
28	818.5	45.7	254	1	CH1T_PETHY
29	817	45.6	253	1	CH1Q_TOBAC
30	784	43.8	253	1	CH1P_TOBAC
31	781.5	43.6	253	1	CH1A_LYCCI
32	766.5	42.8	253	1	CH1A_LYCES
33	765	42.7	316	1	CH18_POPTR

RESULT 1

ID	CH1L_HORVU	STANDARD;	PRT;	318 AA.
AC	P11955;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	26 KDA ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_TaxID=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. NK 1558; TISSUE=Leaf;			
RA	Ignatius S.M.J.; Huang J.; Muthukrishnan S.;			
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 141-318 FROM N.A.			
RC	STRAIN=CV. HIMALAYA;			
RA	Swegli M., Huang J.-K., Lee G., Muthukrishnan S.;			
RT	"Identification of an endochitinase cDNA clone from barley aleurone cells";			
RL	Plant Mol. Biol. 12:403-412(1989).			
CC	FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN			
CC	CONTAINING FUNGAL PATHOGENS.			
CC	CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF			
CC	N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.			
CC	INDUCTION: BY ETHYLENE.			
CC	SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO			
CC	CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL			
CC	CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL			
CC	HYDROLASES).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; U02287; AAA18586.1; -			
DR	EMBL; X15349; CAA33407.1; -			
DR	PIR; S04131; S04131.			
DR	HSSP; P23951; 2BAA.			
DR	InterPro; IPR001002; Chitin_bind.			
DR	InterPro; IPR000726; Glyco_hydro_19.			
DR	Pfam; PF00187; chitin_binding; 1.			
DR	Pfam; PF00182; Glyco_hydro_19; 1.			
DR	PRINTS; PR00451; CHITINBINDING.			
DR	ProDom; PD000574; Glyco_hydro_19; 1.			
DR	ProDom; PD000609; Chitin_bind; 1.			
DR	SMART; SM00270; ChtBD1; 1.			
DR	PROSITE; PS00773; CHITINASE_19_1; 1.			

P11218 urtica dioi
P42820 beta vulgar
P29023 zea mays (m
P29022 zea mays (m
Q06209 brassica na
P27054 phaseolus v
P80052 dioscorea j
P29032 populus tri
P15326 coix lachry
P09762 solanum tub
Q06016 arachis hyp
Q06013 arachis hyp

```
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 318 26 KDA ENDOCHITINASE 1.
FT DOMAIN 20 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 22 37 BY SIMILARITY.
FT DISULFID 31 43 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 53 57 BY SIMILARITY.
SQ SEQUENCE 318 AA; 33402 MW; 42D62B2FE8041954 CRC64;

Query Match 72.4%; Score 1297; DB 1; Length 318;
Best Local Similarity 74.0%; Pred. No. 3.2e-92;
Matches 233; Conservative 27; Mismatches 43; Indels 12; Gaps 3;

QY 12 VLAVLVAAAVTPATAQCQSAGGAKCADCCLCCSQRFCTGTSYDYGPRCQSCCTCGG 71
Db 5 VLFVAVMAAA-TMAVABQCQSAGGATCPNCLCCSRFGWGST-PYCGDGCQSCQCGG 62
QY 72 -----GGGVSASIVSRDLPERLLHRNDAACIARGFYTYDAFLAAGAPPAFGTT 121
Db 63 GSTPVTTPSGGGGVSSIVSRDLPERLLHRNDAACIARGFYTYDAFLAAGAPPAFGTT 122
QY 122 GDLTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCKFOEGSPSPSYCDQSDADWPCAP 181
Db 123 GGTDRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCKFOEGSPSPSYCDQSDADWPCAP 182
QY 182 GKQYVGRPIQLTHNYNGPAGRAIGVVDLLNPNLDVATDPTVAEFTAIWMTQSNKPS 241
Db 183 GKSYVGRPIQLTHNYNGPAGRAIGVVDLLNPNLDVATDPTVAEFTAIWMTQSNKPS 242
QY 242 CHVITGLWPTARDASAGRPVPGVITNVINGIECGMGQNDKVAADRIGFYKRYCPIFG 301
Db 243 SHAVITGQSPSGDRAAGRPVPGVITNVINGIECGMGQNDKVAADRIGFYKRYCPIFG 302
QY 302 IGYNNLDCTNLSF 316
Db 303 VGYNNLDCTNLSF 317

RESULT 2
CHI2_ORYSA
ID CHI2_ORYSA STANDARD; PRT; 336 AA.
AC P25765;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).
GN RCH10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91238706; PubMed=2034221;
RA Zhu Q., Lamb C.J.;
RT "Isolation and characterization of a rice gene encoding a basic
RT chitinase."
RL Mol. Gen. Genet. 226:289-296(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
DR PIR; S15997; S15997.
DR HSSP; P23951; 2BAA.
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DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRIN3; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 336 BASIC ENDOCHITINASE 2.
FT DOMAIN 22 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 24 39 BY SIMILARITY.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 336 AA; 35565 MW; 7F4EC126265DEA84 CRC64;

Query Match 68.6%; Score 1230; DB 1; Length 336;
Best Local Similarity 69.3%; Pred. No. 4.4e-87;
Matches 221; Conservative 31; Mismatches 55; Indels 12; Gaps 3;

QY 4 LRACATCAVLAIVLAAAVTPATAQCQSAGGAKCADCCLCCSQRFCTGTSYDYGPRCQ 63
Db 1 MRALAVAMVAPPLAAAV---HAQCQSAGGAVCNCLCCSQFGWGSTSDYCGAGCQ 57
QY 64 SQCT-----GCGGGGGVASTVSRDLPERLLHRNDAACIARGFYTYDAFLAAGAF 115
Db 58 SQSRLRRRPDASGGGSGVASTVSRSLFDLMLHRNDAACAPASNFYTYDAFAAASAF 117
QY 116 PAFGTTGDLTRKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCKFOEGSPSPSYCDQS 174
Db 118 PGFAAGDADTNKREVAAPFGQTSHTTGGWPTAPDGPFSWGYCKFOEGSPSPSYCDQS 177
QY 175 ADWPCAPGKQYVGRPIQLTHNYNGPAGRAIGVVDLLNPNLDVATDPTVAEFTAIWMT 234
Db 178 AQWPCAAGKQYVGRPIQLTHNYNGPAGRAIGVVDLLNPNLDVATDPTVAEFTAIWMT 237
QY 235 TQSNKPSCHDVITGLWPTARDASAGRPVPGVITNVINGIECGMGQNDKVAADRIGFYK 294
Db 238 PQSPKPSCHNAVATGQWTPSADDDQAGRPVPGVITNVINGIECGMGQNDKVAADRIGFYK 297
QY 295 RYCDIFGIGYGNLDCTNLSF 313
Db 298 RYCDILGVSYGANLDCTNLSF 316

RESULT 3
CHI1_ORYSA
ID CHI1_ORYSA STANDARD; PRT; 318 AA.
AC P24626;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370899; PubMed=1993114;
RA Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
RA Muthukrishnan S., Reeck G.R.;
RT "Nucleotide sequence of a rice genomic clone that encodes a class I
RT endochitinase."
```


Query Match 66.8%; Score 1196.5; DB 1; Length 324;
Best Local Similarity 65.8%; Pred. No. 1.5e-84;
Matches 211; Conservative 42; Mismatches 58; Indels 9; Gaps 3;

QY 1 MSTLRARCATAVLAVVLAANAATPATAEQSGAGKACDCLCCSQFGTSDYCGP 60
DB 1 MSLKLF-----IPILLVLVIFSCCAEQGTQAGALCPGGLCCSKFGWCGSTSEYCGD 53

QY 61 RCQSQTGCGGGGGVYASIVSRDLPRFLLHRNDACIARGFTYDAFLAAAGAFAGT 120
DB 54 GCQSCSG-SSGGGTLSLISDGTFNMLKLRNDACQKPFYTYDAFLSAAKAFNFAN 112

QY 121 TGLDLTRKREVAFFGOTSHETTGWPTADPGFSGYCFKQSGPSPSYCDOSADWPCA 180
DB 113 KGTATKREIAFLAFLQGTSHETTGWPTADPGYANGYCFELRQ-NPSYCYQASSFEPCA 171

QY 181 PGQYVGRGPIQLTHNYNYPAGRA.GVLLNNPDLVADPTVAFKTAIFWMTTQSNKP 240
DB 172 SGQYVGRGPIQTSWNYNQCQCGRAIGVLLNNPDLVADPTVAFKTAIFWMTTQSNKP 231

QY 241 SCHDVITGLWTPARSAAGRVPGYVITNVINGTECGMGQNDKYADRLGFKRYCDIF 300
DB 232 SCHDVITGWTPSSADRAAGRLPGYVITNVINGTECGMGQNDKYADRLGFKRYCDIF 291

QY 301 GIGYGNLDCYNOLSNFVGL 320
DB 292 GIGYGNLDCYSQRPFGSSL 311

RESULT 5
CHIL_SOLUTU STANDARD; PRT; 318 AA.

AC P52403;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTBL.

OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL HYDROLASES).
CC -----
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CC EMBL; U02605; AA18332.1; -
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT NON_TER 1
FT SIGNAL <1 18
FT CHAIN 19 311
FT PROPEP 312 318
FT DOMAIN 19 60
FT DISULFID 21 36
FT DISULFID 30 42
FT DISULFID 35 49
FT DISULFID 54 58
FT SEQUENCE 318 AA; 33813 MW; A0B49DA528706AAA CRC64;

Query Match 66.6%; Score 1193; DB 1; Length 318;
Best Local Similarity 66.8%; Pred. No. 2.8e-84;
Matches 205; Conservative 42; Mismatches 58; Indels 2; Gaps 2;

QY 16 VLAAAAVTATATFQCGSQAGGAKCADCCLCCSQFGTSDYCGP-RCOSQCTGCGGGG 74
DB 7 LLFSVILLASAEQCGSQAGGALCAGLCCSKFGWCGDINDYCGNCSQCGGPGPSG 66

QY 75 GVASIVSRDLFERLLHRNDACIARG-FYTYDAFLAAAGAFAGTGDLDTRKREVA 133
DB 67 DIGGVLSNMFQDLNHRNDACQGNFYNAFISAAGSPFGFTGDTARKREIAA 126

QY 134 FFGQTSHTETGGWPTADPGFSGYCFKQSGPSPSYCDOSADWPCAPGKQYVGRPIQL 193
DB 127 FFAQTSHETTGWPTADPGYANGYCFELRQSGPSPSYCDOSADWPCAPGKQYVGRPIQL 186

QY 194 THNYNYPAGRAIGVLLNNPDLVADPTVAFKTAIFWMTTQSNKPSCHDVITGLWPT 253
DB 187 SHNYNYPGCGRAIGVLLNNPDLVADPTVAFKTAIFWMTTQSNKPSCHDVITGLWPT 246

QY 254 ARDSAGRVPGYVITNVINGTECGMGQNDKYADRLGFKRYCDIFGIGYGNLDCYNQ 313
DB 247 GVDQAANRVPGYVITNVINGTECGMGQNDKYADRLGFKRYCDIFGIGYGNLDCYNQ 306

QY 314 LSPNVGL 320
DB 307 RSPGNGL 313

RESULT 6

CHIL_LYCES STANDARD; PRT; 322 AA.
ID CHIL_LYCES
AC Q05538;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHI9
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]


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EMBL: X51599; CAA35945.1; -
EMBL: X64519; CAA45822.1; -
EMBL: M15173; AAA34070.1; -
PIR: A29074; A29074.
PIR: S13322; S13322.
PIR: S20981; S20981.
HSSP: P23951; 2BAA.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR000726; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS: PR00451; CHITINBINDNG.
ProDom: PD000574; Glyco_hydro_19; 1.
ProDom: PD000609; Chitin_bind; 1.
SMART: SM00270; ChtBD1; 1.
PROSITE: PS00026; CHITIN_BINDING; 1.
PROSITE: PS00773; CHITINASE_19; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
Hydroxylation; Multigene family.
KW
FT SIGNAL 1 23
FT CHAIN 24 317 ENDOCHITINASE B.
FT PROPEP 318 324 REMOVED IN MAURE FORM (PROBABLE).
FT DOMAIN 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION.
FT MOD_RES 69 69 HYDROXYLATION.
FT SEQUENCE 324 AA; 34721 MW; FA65DC2113B33EB6 CRC64;

Query Match 56.1%; Score 1184; DB 1; Length 324;
Best Local Similarity 64.7%; Pred. No. 1.4e-83;
Matches 207; Conservative 46; Mismatches 63; Indels 4; Gaps 3;

QY 4 LRARCATAVLAVLAAAVTATAEQSGAGGAKCADCLCCSQFGCGTSDYCGP-RC 62
Db :| | | | :| | | | | | | | | | | | | | | | | | | | |
1 MRLREFTA-LSSLFSLLLSASAEQCGSQAGGARCASGLCCSKFGCGTNDYCGPGNC 59
QY 63 QSOCTG--CGGGGGVAVSVSRDLFERFLHRNDAACLAGFYDYDAAGAPFAGT 120
Db :| | | | | | | | | | | | | | | | | | | | | | | | | |
60 QSQCPGPTFPFGGDDGSGIISSMFMDQLKRNDAACGKGFVSYNAFINAAFSFPGGT 119
QY 121 TGLDTRKREVAFAFGTSHETTGWPTAPDGPFSWGYCFKQCGSPSYCDQSDAWPCA 180
Db :| | | | | | | | | | | | | | | | | | | | | | | | | |
120 SGTATARKREIAFAAFAQTSHETTGWATPDGPYAWGYCWLREGSGDYCTPSGQWPCA 179
QY 181 PGKYYGGRGPIQLTHNYNYPAGRAIGVDLLNPNLDVATPTVAFTAIFWMTQSNKP 240
Db :| | | | | | | | | | | | | | | | | | | | | | | | | |
180 PGRKYFGRGPIQISHNYPGCRRAIGVDLLNPNLDVATPDVTSFKALFWMTTPQSPKP 239
QY 241 SCHDVITGLTPTARDASAGRVGYVITNVINGIECGQNDKVDADRIGFYKRYCIDF 300
Db :| | | | | | | | | | | | | | | | | | | | | | | | | |
240 SCHDVITGRWQPSADRAANKLPFGVITNIINGGLECGRGTSDRVQDRIGFYKRYCIL 299
QY 301 GYGNNLDYNNQLSFNVL 320
Db :| | | | | | | | | | | | | | | | | | | | | | | | | |
300 GVSFGDNLDCNQSFNGNL 319

RESULT 8
CHIL_TOBAC

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ID AC P08252; STANDARD; PRT; 329 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
GN CHN48.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097; [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV HAVANA 425; TISSUE=Leaf;
RX MEDLINE=91346623; PubMed=1966383;
RA Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr.;
RT "Structure of a tobacco endochitinase gene: evidence that different
RT chitinase genes can arise by transposition of sequences encoding a
RT cysteine-rich domain.";
RL Plant Mol. Biol. 14:357-368(1990).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=92052270; PubMed=1946457;
RA Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
RT targeting of chitinases to the plant vacuole.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
RN [3]
RP HYDROXYLATION.
RX MEDLINE=92358209; PubMed=1496378;
RA Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
RT containing proteins.";
RL Science 257:655-657(1992).
CC -|- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -|- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -|- INDUCTION: BY ETHYLENE.
CC -|- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL: X16938; CAA34812.1; -
EMBL: X16939; CAA34813.1; -
PIR: S08627; S08627.
HSSP: P23951; 2BAA.
InterPro: IPR001002; Chitin_bind.
InterPro: IPR000726; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS: PR00451; CHITINBINDNG.
ProDom: PD000574; Glyco_hydro_19; 1.
ProDom: PD000609; Chitin_bind; 1.
SMART: SM00270; ChtBD1; 1.
PROSITE: PS00026; CHITIN_BINDING; 1.
PROSITE: PS00773; CHITINASE_19; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
Hydroxylation; Multigene family.
KW
FT SIGNAL 1 23
FT CHAIN 24 322 ENDOCHITINASE A.

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FT PROPEP 323 329 REMOVED IN MATURE FORM.
FT DOMAIN 24 55 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION (PARTIAL).
FT MOD_RES 69 69 HYDROXYLATION.
FT MOD_RES 71 71 HYDROXYLATION.
FT MOD_RES 72 72 HYDROXYLATION.
FT MOD_RES 74 74 HYDROXYLATION.
FT MOD_RES 75 75 HYDROXYLATION (PARTIAL).
SEQUENCE 329 AA; 35156 MW; 3EC99D96E6C0114C CRC64;

Query Match 65.9%; Score 1181; DB 1; Length 329;
Best Local Similarity 63.6%; Pred. No. 2.4e-83;
Matches 204; Conservative 44; Mismatches 65; Indels 8; Gaps 2;

QY 8 CATVALVLAARAAVTPATAECGSGAGAKCADLCCSQFGCGTTSYCGP-RQSQSC 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 4 CFTALSSLLFSLLSASAECGSGAGARCPGLCCSKFGWCGNTNDYCGPGNCQSC 63

QY 67 TG-----CGGGGGVASTVSRDLPERLLHENDACIARGTYTDAFLAAGATPAFG 119
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 64 PGGPTPTPTPGGGDLGSLISSMFDQMLKHNDRNACQKGFYSYNAFTNAARSPFGG 123

QY 120 TGGDLTRKREVAAPFGTSHETGWPATDPGPFWSWGYCFKQEGSPSPSCQSDADWPC 179
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 124 TSGDTTARKRETAARFAQTSHETTGWATAPDGPYANGYCWLEQSGPDGYCTPSQWPC 183

QY 180 APCKQYVGGPQLTHNYNGPAGRAIGVDLLNPNPLVATDPTVAKTAIWFWMTQSNK 239
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 184 APERKFGGPIQISHNYNGPGRGIGVDLLNPNPLVATDPTVISEKSAIWFWMTPQSPK 243

QY 240 PSCHDVITGLWPTARDSAAGVPYGVITNYINGIEGGMQNDKVAADRGYKRYCDI 299
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 244 PSCHDVITGRWQPSAGDRANRUPGVITNYINGIEGGRGDSRVQDRIGERYCYSI 303

QY 300 FGIGYGNLDCYNQLSFNVL 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 304 LGVSPGDNLDGNGRSGNGL 324
```

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RESULT 9
CHI3_SOLTU STANDARD; PRT; 318 AA.
AC P52405;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
GN ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerthues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
RT and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
CC SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
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CC SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
CC OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U02607; AAA17409.1; --
CC HSSP: P23951; ZBAA.
CC InterPro: IPR001002; Chitin_bind.
CC InterPro: IPR000726; Glyco_hydro_19.
CC Pfam: PF00187; chitin_binding; 1.
CC Pfam: PF00182; Glyco_hydro_19; 1.
CC ProDom: PD000574; Glyco_hydro_19; 1.
CC ProDom: PD000609; Chitin_bind; 1.
CC SMART: SM00270; ChtBD1; 1.
CC PROSITE: PS00026; CHITIN_BINDING; 1.
CC PROSITE: PS00773; CHITINASE_19_1; 1.
CC PROSITE: PS00774; CHITINASE_19_2; 1.
CC Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Multigene family.
FT NON_TER 1 1 POTENTIAL.
FT SIGNAL <1 18 ENDOCHITINASE 3.
FT CHAIN 19 311 REMOVED IN MATURE FORM, VACUOLAR
FT PROPEP 312 318 TARGETING (POTENTIAL).
FT DOMAIN 19 60 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 21 36 BY SIMILARITY.
FT DISULFID 30 42 BY SIMILARITY.
FT DISULFID 35 49 BY SIMILARITY.
FT DISULFID 54 58 BY SIMILARITY.
FT SEQUENCE 318 AA; 33798 MW; BF587A8515534E71 CRC64;
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Query Match 65.7%; Score 1177; DB 1; Length 318;
Best Local Similarity 67.4%; Pred. No. 4.7e-83;
Matches 201; Conservative 40; Mismatches 55; Indels 2; Gaps 2;

QY 25 ATAEQCGSAGGAKCADLCCSQFGCGTTSYCGP-RQSQCTGCGGGGGVASTVSRD 83
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 16 ASAEQCGSAGGALCAPGLCCSKFGWCGNTNDYCGPGNCQSCPGGPGSDIGGVINS 75

QY 84 LFERFLHRNDAACIAR-GFYTYDAFLAAGAPPAFGTTGDLTRKREVAAPFGTSHET 142
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 76 MFDQMLNHRNDRNACQKKNFYSYNAFISAGSPFGTGTGTARRETAARFAAQSHET 135

QY 143 TGGWPTAPDGPFSWGYCFKQEGSPSPSCQSDADWPCAPKQYVGGPQLTHNYNGPA 202
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 136 TGGWPSAPDGPYANGYCFELREQSGPDGYCTPSSQWPCAPERKYVGGPQLTHNYNGPC 195

QY 203 GRAIGVDILNPNPLVATDPTVAKTAIWFWMTQSNKPSCHDVITGLWPTARDSAAGRV 262
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 196 GRAIGVDLLNPNPLVATDPTVISEKSAIWFWMTPQSPKPSCHDVITGRWQPSAGDQANRV 255

QY 263 PGYGVITNVIINGIEGGMQNDKVAADRGYKRYCDIFGIGYGNLDCYNQLSFNVL 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 256 PFGVITNVIINGIEGCHGSDRSRVQDRIGFYRYCGILGVSPGDNLDGNGRSGNGL 313

RESULT 10
CHI2_SOLTU STANDARD; PRT; 316 AA.
ID CHI2_SOLTU
AC P52404;
DT 01-OCT-1996 (Rel. 34, Created)
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DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 321 ENDOCHITINASE 1.
FT DOMAIN 22 62 CHITIN-BINDING (BY SIMILARITY).
FT DOMAIN 63 98 HINGE.
FT DOMAIN 99 321 CATALYTIC.
FT DISULFID 24 39 BY SIMILARITY.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 38 52 BY SIMILARITY.
FT DISULFID 58 62 BY SIMILARITY.
SQ SEQUENCE 321 AA; 34847 MW; E87DBEBC8D7A2ADB CRC64;

Query Match 65.1%; Score 1166; DB 1; Length 321;
Best Local Similarity 69.1%; Pred. No. 3.2e-82;
Matches 206; Conservative 33; Mismatches 53; Indels 6; Gaps 4;

QY 26 TAEQCGSQAGGAKADCLCCSQFGCGTSDYCGPR--CQSQCTGCGGGGGVASTVSRD 83
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 SAEQCGRQAGALCPGLCCSQFGCGGNDYCKKENGCCQSCGSGGDTGGLDSLITRE 79
QY 84 LFERELHRNDACLARGFYTYDAFLAAGAPFAFGTGLDTRKREVAFAFGTSHETT 143
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 RFDQMLHRNDGGCPARGFYTYDAFLAAGAPFAFGTGLDTRKREVAFAFGTSHETT 139
QY 144 G--GWPTAPDGPFFSWGKCFKQEGSPSYCDQSDADWPCAPGKQYIGRPIOLTHYNYGP 201
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 GGAGW-AAPDGPYTWGVCYNREL-NPADIQWMDPNYPCAPGKQYEGRGMOLTYNYGQ 197
QY 202 AGRAIGVDLLNPNDLVATDPTAFKTAIWMTTQSNKPSCHDVTITGLWPTARDASAGR 261
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
198 CGRAIGVDLLNPNDLVATDPTISFSAFWMTTQSNKPSCHDVTITGLWPTARDASAGR 257
QY 262 VPGVGVTNVIINGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNLDCYNQLSFFNVG 319
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 VPGFGLTNIINGLEGCGMGNAQVEDRIGFYKRYCDITLGVGYGNLDCYNQRSYNNG 315

RESULT 12
CHIL_GOSHI
ID CHIL_GOSHI STANDARD; PRT; 324 AA.
AC Q39799;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
NCBI_TaxID=3635;
[1]
SEQUENCE FROM M.A.
RC STRAIN=CV; COKER 201;
RA Leverson J.F.; Chlan C.A.;
RT "Isolation of a genomic DNA clone from Gossypium hirsutum with high
RL similarity to class I endochitinase plant sequences.";
RL (In) Plant Gene Register PGR96-054.
CC -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC -!- N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC -----
CC EMBL; U60197; AAB67842.1; -.
DR HSSP; P02877; IHEV.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 317 ENDOCHITINASE 1.
FT PROPEP 318 324 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 23 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 25 40 BY SIMILARITY.
FT DISULFID 34 46 BY SIMILARITY.
FT DISULFID 39 53 BY SIMILARITY.
FT DISULFID 58 62 BY SIMILARITY.
SQ SEQUENCE 324 AA; 34666 MW; 9923B123EF5C7E3E CRC64;

Query Match 64.9%; Score 1163; DB 1; Length 324;
Best Local Similarity 65.5%; Pred. No. 5.5e-82;
Matches 207; Conservative 41; Mismatches 62; Indels 6; Gaps 4;

QY 11 AVLAVLAAAAVTATATACGCGSQAGGAKADCLCCSQFGCGTSDYCG-PRCSQCTGC 69
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
6 ALSTFLLLLIVVVGSAEQCGRQAGALCPGLCCSQFGCGSTADYCTVPGCSQCSGS 65
QY 70 G--GGGGVASIVSRDLFRFLHRNDAAALARGFYTYDAFLAAGAPFAFGTGLDTR 127
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 GPAPGPGGLTNLSRETFNQMLLHRNDGACPARGFYTYDAFLAARSPFAFGTGDQATR 125
QY 128 KREVAFAFGTSHETT--GWPTAPDGPFFSWGKCFKQEGSPSYCDQSDADWPCAPGKQY 185
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 KREIAFAFIAOTSHETTGGAGW-AAPDGPYAWGVCYNRELNPSPSYCYASDPNYPACPKQY 184
QY 186 YGRGPIOLTHYNYGYPAGRAIGVDLLNPNDLVATDPTAFKTAIWMTTQSNKPSCHDV 245
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 FGRGPMLSNWNYNVGCGRAIGVDLLNPNDLSSDPTISFSAFWMTTQSNKPSCHDV 244
QY 246 ITGLWPTARDASAGRVPYGVYTNVIINGIECGMGQNDKVADRIGFYKRYCDIFGIGY 305
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 IIGAWSPSSSDRAAGRPVGYGVITNIINGLEGCGMGNAQVEDRIGFYKRYCDILGVSYG 304
QY 306 NNLDCYNQLSFFNVGLA 321
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
305 NNLDCYNQSPFGNGVS 320

RESULT 13
CHIT_ARATH
ID CHIT_ARATH STANDARD; PRT; 322 AA.
AC P19171;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN MQC3.32
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;

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Db	63	GGTPPGPTDLSGISSSDFDDMLKHNDAACPARGFYTNATITAAKSPFGFTGDTA	122
QY	126	TRKREVAAPFGQTSHEHTGWTPAPGSPSWGVCYCFKOEQSPSPSYCDQSDADWFCAPGQY	185
Db	123	TRKREVAAPFGQTSHEHTGWTPAPGSPSWGVCYCFKOEQNPASDYCEPSATWPCASGKRY	182
QY	186	YGRGPTQLTHNYNYGPAIGRAIGVDLLNNPDLVATDPTVAFTKAIWFMMWTQSNKPSCHDV	245
Db	183	YGRGPMQLSNWNYGCGRAIGVDLLNNPDLVANDAVIAFAKAIWFMMTAQPPKPSCHAV	242
QY	246	ITGLWTPARDASAGRPVPGYGVITNVINGIECGMQNDKVADRIGFYKRYCDIFIGYGV	305
Db	243	IAGOWPSPDADRAAGKMLPGYGVITNIINGLEGRGQGVADRIGFYGRYCNIFGVNPG	302
QY	305	NNLDCYNQLSFNVL	320
Db	303	GNLDCYNQRSFVNL	317
RESULT 14			
ID	CH12_BRANA	STANDARD;	PRT; 322 AA.
AC	Q09023;		
DT	01-OCT-1994 (Rel. 30, Created)		
DT	01-OCT-1994 (Rel. 30, Last sequence update)		
DT	01-OCT-1994 (Rel. 30, Last annotation update)		
DE	ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).		
OS	Brassica napus (Rape).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eucrodis II; Brassicales; Brassicaceae; Brassica.		
OX	NCBI_TaxID=3708;		
RP	[1]		
FN	SEQUENCE FROM N.A.		
FX	MEDLINE=94143492; PubMed=8310072;		
RA	Hamel F., Bellemare G.;		
RT	"Nucleotide sequence of a Brassica napus endochitinase gene. ";		
RL	Plant Physiol. 101:1403-1403(1993).		
CC	-!- CATALYTIC ACTIVITY: HYDROLYSES OF		
CC	N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN		
CC	-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO		
CC	CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL		
CC	CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL		
CC	HYDROLASES).		

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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; M95835; AAA32986.1; -		
DR	HSSP; P23951; 2BAA.		
DR	InterPro; IPR001002; Chitin_Bind.		
DR	InterPro; IPR000726; Glyco_hydro_19.		
DR	Pfam; PF00187; chitin_binding_1.		
DR	Pfam; PF00182; Glyco_hydro_19; 1.		
DR	PRINTS; PR00451; CHITINBINDNG.		
DR	ProDom; PD000574; Glyco_hydro_19; 1.		
DR	ProDom; PD000609; Chitin_bind; 1.		
DR	SMART; SM00270; ChtBD1; 1.		
DR	PROSITE; PS00026; CHITIN_BINDING; 1.		
DR	PROSITE; PS00773; CHITINASE.19.1; 1.		
DR	PROSITE; PS00774; CHITINASE.19.2; 1.		
KW	Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;		
KW	Multigene family.		
FT	SIGNAL	1	20
FT	CHAIN	21	322
FT	DOMAIN	21	62
FT	DISULFID	23	48
FT			BY SIMILARITY
FT			CHITIN-BINDING (BY SIMILARITY)
FT			POTENTIAL.
FT			ENDOCHITINASE CH25.

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FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
SQ SEQUENCE 322 AA; 34816 MW; E62EE4B17211DBCD CRC64;

Query Match
Best Local Similarity 64.0%; Score 1146; DB 1; Length 322;
Matches 205; Conservative 34; Mismatches 68; Indels 2; Gaps 2;

QY 10 TAVLVVLAATAVTPATAECGSAAGKACDCLCGSQFQCGTSDYC-GPRCQSQCTG 68
Db 3 SCLELLIFSLFSFSLAECCGQAGALCPNGLCCSEFGWCGDTAYCKQPCQSQCGG 62
QY 69 C-CGGGGGVASIVSRDLFRFLHRNDACLAGFYTYDAFLAAAGAFPAFGTGLDTR 127
Db 63 TPGPTGDLGSIISQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGFGTGTATR 122
QY 128 KREVAFFGOTSHETTGMPADPGFSGYCFKQKQSGPPSYCDOSADWPAPGQYIG 187
Db 123 KKLIAFFGOTSHETTGMPADPGFSGYCFKQKQSGPPSYCDOSADWPAPGQYIG 182
QY 188 RGPQITHTNNYAGPAGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVIT 247
Db 183 RGPQISLWNNYAGPAGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVIT 242
QY 248 GLWTPPTARDASAGRVPGYVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIGYNN 307
Db 243 GOWQPSDADRAAGRVPGYVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIGYNN 302
QY 308 LDCYNQLSF 316
Db 303 LDCYNQRSF 311
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RESULT 15
CHIX_PEA
ID CHIX_PEA STANDARD; PRT; 320 AA.
AC P36907;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE ENDOCHITINASE PRCURSOR (EC 3.2.1.14).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BIRIE; TISSUE=Leaf;
RA Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
RA Collinge D.B.;
RT "Accumulation of defence-related transcripts and cloning of a
RT chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with
RT Ascochyta pisi lib.,"
RL Plant Sci. 92:69-79(1993).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC -!- CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- INDUCTION: BY FUNGAL INFECTION.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC or send an email to license@isb-sib.ch.
CC -----
DR EMBL: X63899; CAA45359.1; -
DR HSSP: P02877; 1HEV.
DR InterPro: IPR001002; Chitin_bind.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam: PF00187; chitin_binding_1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR PRINTS: PR00451; CHITINBINDNG.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR ProDom: PD000609; Chitin_bind; 1.
DR SMART: SM00270; CHUBD1; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 320 ENDOCHITINASE.
FT DOMAIN 24 64 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 58 62 BY SIMILARITY.
SQ SEQUENCE 320 AA; 34507 MW; 7EDEC8C1AEECC3435 CRC64;

Query Match
Best Local Similarity 63.9%; Score 1145.5; DB 1; Length 320;
Matches 202; Conservative 32; Mismatches 55; Indels 9; Gaps 2;

QY 27 AEQCSQAGGAKACDCLCGSQFQCGTSDYCGPRCQSQCTGC-----GGGGGGVAS 78
Db 23 AEQCSQAGGAVCPNGLCCSKGFCGSTDYCGDGCQSQCKSPPTFTPTSTGGDVGVR 82
QY 79 IYSRDLFERFLHRNDACLAGFYTYDAFLAAAGAFPAFGTGLDTRKREVAAPFGOT 138
Db 83 LVPSSLFQDLKRYRNDGRGAGHGFYTYDAFLAAARSFNGFGTGGDDTKKELAAFLAQT 142
QY 139 SHETTGGWPTAPDGPFSWGVCFKQEQSPSYCDQSDADWPCAPKQYGYGPIOLTHNN 198
Db 143 SHETTGGWPTAPDGPYANGYCFVSEGTQEVYCSPK-DWPCAPGKKYGRGPIQLTHNN 201
QY 199 YGPAGRAIGVLLNPNLDVATDPTVAFKTAIWFWMTQSNKPSCHDVITGLWTPPTARDSA 258
Db 202 YGLAGQAIKEDLINPDLLSTNPFVSEKTAIWFWMTQSNKPSCHDVITGRWTPSAADSS 261
QY 259 AGRVPGYGVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIGYNNLDYNNQLSF 316
Db 262 AGRVPGYGVITNVINGIECGMGQNDKVDRIFGFYKRYCDIFGIGYNNLDYNNQLSF 319
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Search completed: May 3, 2002, 18:48:32
Job time: 916 sec

1


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Db 61 CGGGTPTPTTPSGGGVSSVSRALEFDRMLLRNDGACQAKGFTYDAFAAAGAPP 120
QY 117 AFGTTGDLTRKREVAARFGQTSHTTGWPTAPDGPFSWGYCFKQEQSPSPSCDSAD 176
Db 121 GFGTTGDTTRKREVAARFLAQTSHTTGWATAPDGAFAWGYCFKQERGATSNYCPSAQ 180
QY 177 WPCAGKQYGRGPIQLTHNYNYPAGRAIGVDLLNPNPLVATDPTVAPKTAIWFWMTQ 236
Db 181 WPCAPKSYGRGPIQLSHNYNYPAGRAIGVDLLRNPLVATDPTVSFKTAMFWMTAQ 240
QY 237 SNKPSCHDVITGLWPTARDASAGRVPGYGVITNVINGIEGGMQNDKADRIQFYKRY 296
Db 241 AKPSPSHAVITGQWSPSTDAAGRVPGYGVITNVINGIEGGMQNDKADRIQFYKRY 296
QY 297 CDIFGIGYGNLDYCNQLSF 316
Db 301 CDILRVGYGNLDYCNQRP 320

RESULT 2
Q43294 PRELIMINARY; PRT; 340 AA.
AC Q43294;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
DE ACETYLGUCOSAMINIDASE (POLY-BETA-GLUCOSAMINIDASE).
GN CHIAL OR CHT-2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPONICA, CV. NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
RT of rice chitinase genes.";
RL Mol. Gen. Genet. 241:1-10(1993).
CC -! CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X56787; CA840107.1; -;
DR EMBL; D16222; BA03750.1; -;
DR HSSP; P23951; 2BAA.
DR Mendel; 727; Oryza; Chial; 727.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitinBd1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 340 CHITINASE.
SQ SEQUENCE 340 AA; 35586 MW; 642F1E3928CA7BE CRC64;

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Query Match 74.0%; Score 1326.5; DB 10; Length 340;
Best Local Similarity 70.9%; Pred. No. 1.1e-111;
Matches 241; Conservative 29; Mismatches 53; Indels 17; Gaps 3;

QY 1 MSTLRARCAT- - - - -VLAVLAAAVTPATAECGSAQAGKACADLCSCQFGFCGTT 55
Db 1 MSTFRAAASLAKKAAIALVALAALATAARACGGAQAAGACPCNCLCCRWGCGTTS 60

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QY 56 DYCGPRCQSQCTGCG- - - - -GGGGVASIVSRDLFFERLLHRNDAAACLAGFETYDA 107
Db 61 DFCGDCQSQCGCGTPTPTPPSPDGVGSIVPRDLFFERLLHRNDGACPARGFYIEA 120
QY 108 FLAAAGAFPAFGTGTGLDTRKREVAARFGQTSHTTGWPTAPDGPFSWGYCFKQEQSP 167
Db 121 FLAAAAAFPAFGTGTGTETKREVAARFGQTSHTTGWPTAPDGPFSWGYCFKQEQNP 180
QY 168 PSYCDQADWPCAPKQYGRGPIQLTHNYNYPAGRAIGVDLLNPNPLVATDPTVAFKT 227
Db 181 SDYQSPSEWPCAPKQYGRGPIQLSFNFYGPAGRAIGVDLLNPNPLVATDPTVSFKT 240
QY 228 ALWFMWTTQSNKPSCHDVITGLWPTARDASAGRVPGYGVITNVINGIEGGMQNDKVA 287
Db 241 ALWFMWTEGGRKPSHVDITGRWAPSPADAAGRAPGYGVITNVINGIEGGMQNDKVA 300
QY 288 DRIGFYKRYCDIFGIGYGNLDYCNQLSFN- - -VGLAAQ 323
Db 301 NRIGFYQRYCGAFGIGTGGNLDYCNQRPFGSSVGLAEQ 340

RESULT 3
Q9SOL3 PRELIMINARY; PRT; 320 AA.
ID Q9SOL3
AC Q9SOL3;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CHITINASE.
GN CH12.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poae; Poa.
OX NCBI_Taxid=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000966; AAF04454.1; -;
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitinBd1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 320 AA; 33711 MW; BEFC3ADBEC939B5 CRC64;

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Query Match 73.5%; Score 1317.5; DB 10; Length 320;
Best Local Similarity 72.6%; Pred. No. 6.7e-111;
Matches 228; Conservative 33; Mismatches 44; Indels 9; Gaps 1;

QY 12 VLAVLAAAVTPATAECGSAQAGKACADLCSCQFGFCGTTSDYCGPRCQSQCTGCG 71
Db 5 VVVTILVAFAVSAHAECGSAQAGGATCPNCLCCKSKFCGCTTSDYCGTQCGQCNCSCG 64
QY 72 - - - - -GGGGVASIVSRDLFFERLLHRNDAAACLAGFETYDAFLAAAGAPPAFGTTG 122
Db 65 PTPVTPPSGGGGVSSIVSGLFEQMLLRNDAAACLAGFETYDAFLAAANSAGFGTTG 124
QY 123 DLDTKREVAARFGQTSHTTGWPTAPDGPFSWGYCFKQEQSPSPSCDSADWPCAPG 182
Db 125 STDVRKREVAARFLAQTSHTTGWPTAPDGPFSWGYCFKQEQGATSDYCSFSSQWPCAPG 194

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RC STRAIN-CV. HASS; TISSUE-MESOCARP;
RA Sowka S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
RA Peterbauer C., Scheiner O., Breiteneder H.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 278202; CAB01591.1; -.
DR HSSP; P02877; IHEV.
DR Mendel; 14766; Perae; Chial; 14766.
DR InterPro; IPR001002; Chitin_bind.
DR Pfam; PF00187; chitin_binding; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 25
FT CHAIN 26 326 ENDOCHITINASE.
SQ SEQUENCE 325 AA; 34586 MW; 643B20589E062E61 CRC64;

Query Match 70.1%; Score 1256; DB 10; Length 326;
Best Local Similarity 69.8%; Pred. No. 2.4e-105;
Matches 220; Conservative 36; Mismatches 55; Indels 4; Gaps 2;

QY 12 VLAVLAAAVTPATAECGSGOAGGAKCADCLCCSQFGCGTTSYDYGPRCQSQCTG-CG 70
DB 10 LLLLLLVLLAGEFAECGQGAGALCPGLCCSQFGCGTTSYDYGPRCQSQCGVTP 69
QY 71 GGGGVASIVSRDLFERFLHRNDAACIARGFYTYDAFLAAAGAFPAFGTTGDLTKRE 130
DB 70 SPGGGVASLISQSFVNMKLRNDAACQAKGYTYNAFIAAANSFNGSVGDTATKRE 129
QY 131 VAAEFGQTSHTTGGWPTAPDPGSPWGYCEKQEGSPSCDQADWPCAPGKQYGRGP 190
DB 130 IAAFLAQISHETGWNATPPDGPYAWGYCFLKEQGNPFDPVCTAOWCAPGKQYGRGP 189
QY 191 IQLTNYNYGPAGRAIGVLDLNNPDVATPTVAFKTAIWFMTTQSNKPSCHDVITGLW 250
DB 190 IQISYNYNYGPAGRAIGVLDLNNPDVATPTVAFKTAIWFMTTQSNKPSCHDVITGLW 249
QY 251 TPTARSDAAGRPVGYGVITNYINGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNLDC 310
DB 250 TPTAARDRAAGRLPGYGVITNYINGIECGMGKFNKVDADRIGFYKRYCDILGVSYGNLDC 309
QY 311 YNQLSFNVG---LAA 322
DB 310 YNORSFGVSTNPLAA 324

RESULT 11
Q9SOL4
ID Q9SOL4 PRELIMINARY; PRT; 340 AA.
AC Q9SOL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-
DE POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHITINASE.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GIADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000964; AAF04453.1; -.

RC STRAIN-CV. HASS; TISSUE-MESOCARP;
RA Sowka S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
RA Peterbauer C., Scheiner O., Breiteneder H.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 278202; CAB01591.1; -.
DR HSSP; P02877; IHEV.
DR Mendel; 14766; Perae; Chial; 14766.
DR InterPro; IPR001002; Chitin_bind.
DR Pfam; PF00187; chitin_binding; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 25
FT CHAIN 26 326 ENDOCHITINASE.
SQ SEQUENCE 325 AA; 34586 MW; 643B20589E062E61 CRC64;

Query Match 70.0%; Score 1254; DB 10; Length 340;
Best Local Similarity 69.3%; Pred. No. 3.8e-105;
Matches 219; Conservative 40; Mismatches 45; Indels 12; Gaps 3;

QY 12 VLAVLAAAVTPATAECGSGOAGGAKCADCLCCSQFGCGTTSYDYGPRCQSQCTGCG 71
DB 6 VVAILVAAFAVS-AHAECGSGOAGGATPCNCLCCSKFGCGTTSYDYGTCGQSQCNCGSG 64
QY 72 -----GGGGVASIVSRDLFERFLHRNDAACIARGFYTYDAFLAAAGAFPAFGTTG 122
DB 65 PTPVTPTPSGGGGVSLVSQLFEQMLHRNDPSCQANGFYTYKAFIAAANSFAGFGTTG 124
QY 123 DLTRKREVAAPFGQSHETTGGWPTAPDPGSPWGYCEKQEGSPSCDQADWPCAPG 182
DB 125 STDVKKREVAAPFAAQSHETTGGWPTAPDPGYSWGYCYKQEGATSDYCSFSSOWPCAPG 184
QY 183 KQYGRGPQLTHNYNYGPAGRAIGVLDLNNPDVATPTVAFKTAIWFMTTQSNKPS 242
DB 185 KKYFGEGPIQISYNYNYGPAGRAIQITDLNNPDVATVSNATVSEFALFWMTAQSPKPS 244
QY 243 HDVITGLWPTARSDAAGRPVGYGVITNYINGIECGMGQNDK-VADRIGFYKRYCDIF 300
DB 245 HAVITGWSPPSSDAQAGRPVGYGVITNYINGIECGMGQNDK-VADRIGFYKRYCDIF 304
QY 301 GIGYGNLDCYNLSF 316
DB 305 GVSYGDLDCYNESPF 320

RESULT 12
Q42993
ID Q42993 PRELIMINARY; PRT; 323 AA.
AC Q42993; Q42996;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-
DE POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIA1 OR CHT-1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RA "Sequence variation, differential expression and chromosomal location
RT of rice chitinase genes."
RL Mol. Gen. Genet. 241:1-10(1993).
RN [2]
RP SEQUENCE OF 21-323 FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA Nishizawa Y., Hibi T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000964; AAF04453.1; -.
DR Plant Sci. 76:211-218(1991).
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DR ProDom: PD000574; Glyco_hydro_19; 1.
 DR SMART: SM00270; Chitinase_19; 1.
 DR PROSITE: PS00773; CHITINASE_19.1; 1.
 DR PROSITE: PS00774; CHITINASE_19.2; 1.
 DR PROSITE: PS00026; CHITIN_BINDING; 1.
 KW Chitin-binding; Signal.
 FT NON_TER <1 17
 FT SIGNAL 18 302
 FT CHAIN 18 302
 FT CHITINASE.
 SQ SEQUENCE 302 AA; 31728 MW; D0687D330BFFD75F CRC64;

Query Match 56.5%; Score 1192; DB 10; Length 322;
 Best Local Similarity 67.2%; Pred. No. 1.4e-99;
 Matches 209; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

QY 16 VLAAAVTATAPAOAGGAGGACADLCCSQFGCGTTSYDYGPRCQSQCT- 67
 DB 2 VITPALEFTNSAQCGGSGALCSNGLCCSQYGYCGNGPGYCGTCQCGGPGGSG 61
 QY 76 VASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAGAPPAFTGTGDLDTKREVAAPF 135
 DB 62 VASIISSLEFQMLHRNDAAACAPANGFYTIDAFIAAANSESGFTGTDTQKRELAAPF 121
 QY 136 GOTSHTTGGWPTAPDPFSGYCFKQEGSQFSGCGTTSYDYGPRCQSQCT- 195
 DB 122 AGTSHTTGGWASAPDPFSGYCFKQEGSQFSGCGTTSYDYGPRCQSQCT- 181
 QY 196 NYNYGAGRAIGVDLNNPDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLWTPTAR 255
 DB 182 NYNYGCGNAINQDLNNPDVADPAISPKTAIFWMTTQSNKPSCHDVITGLWTPTAR 241
 QY 256 DSAAGRVPGYGVITNVINGTECGMGONDVADRIKGYKCYDIFGIGYNNLDYCNQLS 315
 DB 242 DQAAERVFPGYGVITNVINGTECGMGONDVADRIKGYKCYDIFGIGYNNLDYCNQLS 301
 QY 316 F 316
 DB 302 F 302

DR ProDom: PD000574; Glyco_hydro_19; 1.
 DR SMART: SM00270; Chitinase_19; 1.
 DR PROSITE: PS00773; CHITINASE_19.1; 1.
 DR PROSITE: PS00774; CHITINASE_19.2; 1.
 DR PROSITE: PS00026; CHITIN_BINDING; 1.
 KW Chitin-binding; Signal.
 FT NON_TER <1 17
 FT SIGNAL 18 302
 FT CHAIN 18 302
 FT CHITINASE.
 SQ SEQUENCE 302 AA; 31728 MW; D0687D330BFFD75F CRC64;

Query Match 56.5%; Score 1204; DB 10; Length 302;
 Best Local Similarity 69.4%; Pred. No. 1.1e-100;
 Matches 209; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

QY 16 VLAAAVTATAPAOAGGAGGACADLCCSQFGCGTTSYDYGPRCQSQCT- 75
 DB 2 VITPALEFTNSAQCGGSGALCSNGLCCSQYGYCGNGPGYCGTCQCGGPGGSG 61
 QY 76 VASIVSRDLFERFLHRNDAAACLARGFYTYDAFLAAGAPPAFTGTGDLDTKREVAAPF 135
 DB 62 VASIISSLEFQMLHRNDAAACAPANGFYTIDAFIAAANSESGFTGTDTQKRELAAPF 121
 QY 136 GOTSHTTGGWPTAPDPFSGYCFKQEGSQFSGCGTTSYDYGPRCQSQCT- 195
 DB 122 AGTSHTTGGWASAPDPFSGYCFKQEGSQFSGCGTTSYDYGPRCQSQCT- 181
 QY 196 NYNYGAGRAIGVDLNNPDVATDPTVAFKTAIFWMTTQSNKPSCHDVITGLWTPTAR 255
 DB 182 NYNYGCGNAINQDLNNPDVADPAISPKTAIFWMTTQSNKPSCHDVITGLWTPTAR 241
 QY 256 DSAAGRVPGYGVITNVINGTECGMGONDVADRIKGYKCYDIFGIGYNNLDYCNQLS 315
 DB 242 DQAAERVFPGYGVITNVINGTECGMGONDVADRIKGYKCYDIFGIGYNNLDYCNQLS 301
 QY 316 F 316
 DB 302 F 302

Search completed: May 3, 2002, 18:47:01
 Job time: 885 sec

RESULT 15
 Q42995 PRELIMINARY; PRT; 322 AA.
 ID Q42995
 AC Q42995;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-
 DE ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
 GN CHIA1 OR RC24.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriophytaceae; Oryzoideae; Oryza.
 OX NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IR36; TISSUE=LEAF;
 RX MEDLINE=96189256; PubMed=8605293;
 RA Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
 RT "Regulation, expression and function of a new basic chitinase gene in
 RT rice (Oryza sativa L.).";
 RL Plant Mol. Biol. 30:387-401(1996).
 CC -/- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
 CC ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 DR EMBL; X87109; CAA60590.1; -;
 DR HSSP; P23951; 2BAA.
 DR Mendel; 1634; Oryza; Chit1; 1634.
 DR InterPro; IPR001002; Chitin bind.
 DR InterPro; IPR000726; Glyco_hydro_19.
 DR Pfam; PF00187; chitin_binding; 1.
 DR Pfam; PF00182; Glyco_hydro_19; 1.

GenCore version 4.5
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 OM protein - protein search, using sw model
 Run on: May 3, 2002, 18:30:30 ; Search time 117.39 Seconds
 (without alignments)
 201.290 Million cell updates/sec

Title: US-09-534-229c-3
 Perfect score: 1765
 Sequence: 1 MRGVVVVAMLAFAFVSAHA.....DLGLVSYGNDLDCYNQRPFA 319

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_ll01.*

- 1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT*
- 2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT*
- 3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT*
- 4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT*
- 5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT*
- 6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT*
- 7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT*
- 8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT*
- 9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT*
- 10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT*
- 11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT*
- 12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT*
- 13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT*
- 14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT*
- 15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT*
- 16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT*
- 17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT*
- 18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT*
- 19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT*
- 20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT*
- 21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT*
- 22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1765	100.0	319	22	AA11489
2	1688.5	95.7	318	20	AAW98079
3	1597.5	90.5	298	20	AAW98080
4	1301.5	73.7	336	13	AAW98019
5	1301.5	73.7	336	16	AAW97969
6	1294.5	73.3	323	22	AA11488
7	1291.5	73.2	336	22	AAW67444
8	1270.5	72.0	329	12	AA15841
9	1256.5	71.2	331	12	AA11305
10	1252	70.9	324	12	AA13225
11	1252	70.9	324	18	AAW31297

12	1252	70.9	324	21	AAW07513	Amino acid sequenc
13	1202.5	68.1	328	13	AAW20822	Sequence of endoch
14	1202.5	68.1	329	15	AAW58860	Endochitinase pr
15	1192.5	67.6	317	17	AAW00186	American elm chit
16	1156	65.5	292	18	AAW24554	Chitinase. Cucur
17	1132.5	64.2	303	13	AAW20820	Sequence of a 302
18	1125	63.7	266	15	AAW52577	Chitinase G. Hord
19	1066	60.4	328	19	AAW64776	Floral organ-speci
20	1003	56.8	2466	20	AAW05844	Banana ripening fr
21	927	52.5	243	20	AAW90169	C. ensiformis chit
22	805.5	45.6	254	12	AAW13274	Petunia extracellu
23	805.5	45.6	254	18	AAW31296	Petunia hybrida ex
24	805.5	45.6	254	21	AAW07512	Amino acid sequenc
25	804.5	45.6	284	21	AAW18905	A maize chitinase
26	794	45.0	439	13	AAW28150	Sugar beet chitina
27	786.5	44.6	272	21	AAW28415	Arabidopsis thalia
28	786.5	44.6	280	21	AAW28414	Arabidopsis thalia
29	777.5	44.1	253	16	AAW76714	Tobacco endochitin
30	777	44.0	259	21	AAW18902	A maize chitinase
31	769.5	43.6	252	21	AAW18903	A maize chitinase
32	757	42.9	252	20	AAW98081	Rye chitinase-like
33	756	42.8	230	20	AAW98082	Rye chitinase-like
34	734	41.6	256	22	AAW11487	Wheat chitinase pr
35	722.5	40.9	372	22	AAW28788	Protein encoded by
36	710.5	40.3	250	16	AAW76713	Wild tomato endoch
37	710.5	40.3	253	16	AAW76712	Wild tomato endoch
38	618	35.0	281	21	AAW18894	A maize chitinase
39	612.5	34.7	155	21	AAW18906	Amino acid sequenc
40	602	34.1	271	21	AAW18904	A maize chitinase
41	602	34.1	271	21	AAW18936	Amino acid sequenc
42	597.5	33.9	268	13	AAW28147	Sugar beet chitina
43	563	31.9	264	13	AAW28145	Sugar beet chitina
44	515.5	29.2	261	21	AAW18896	A maize chitinase
45	504.5	28.6	813	21	AAW53657	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AA11489

ID AA11489 standard; protein; 319 AA.

XX

AC AA11489;

XX

DT 02-MAR-2001 (first entry)

XX

DE Wheat chitinase protein homologous to spring wheat chitinase.

XX

KW Wheat; chitinase; low temperature expression; hardened; plant;

XX

XX snow mould resistance; psychophilic plant pathogen; spring wheat.

OS Triticum aestivum.

XX

PN JP2000270866-A.

XX

PD 03-OCT-2000.

XX

PF 25-MAR-1999; 99JP-0081694.

XX

PR 25-MAR-1999; 99JP-0081694.

XX

PA (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

XX

DR WPI; 2001-027417/04.

XX

PT New low temperature expression chitinase gene for producing a plant

XX

XX grade highly resistant to psychophilic plant pathogenic microbes

PS Claim 7; Fig 3; 11pp; Japanese.

XX

CC This invention describes novel wheat chitinase genes. The invention also

OC describes a method for the isolation of a low temperature expression

CC chitinase gene in which the mRNA is extracted from a fully hardened
 CC autumn wheat P1173438 (of high snow mould resistance). The genes are
 CC useful for creating a plant grade, highly resistant to psychophilic plant
 CC pathogenic microbes.
 CC
 XX Sequence 319 AA;

Query Match 100.0%; Score 1765; DB 22; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1.1e-137;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 DB 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 QY 61 GCSGGTVPVPTPSGGVSSISQSLFDQMLLRNDACIAKAGFYNGAFVAAANSFSGF 120
 DB 61 GCSGGTVPVPTPSGGVSSISQSLFDQMLLRNDACIAKAGFYNGAFVAAANSFSGF 120
 QY 121 ATGSTDVKKREVAFLAQTHSHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 180
 DB 121 ATGSTDVKKREVAFLAQTHSHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 180
 QY 181 CAPGKKYFGRGPIQISHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 240
 DB 181 CAPGKKYFGRGPIQISHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 240
 QY 241 KPSSHDTVTRWSPSGADQAAGRPVGYVTNINGLGECGRGDGRVADRIGFYKRYCD 300
 DB 241 KPSSHDTVTRWSPSGADQAAGRPVGYVTNINGLGECGRGDGRVADRIGFYKRYCD 300
 QY 301 LLGVSYGDNLDYCNQRPFA 319
 DB 301 LLGVSYGDNLDYCNQRPFA 319

RESULT 2
 AAW98079
 ID AAW98079 standard; Protein; 318 AA.
 XX
 AC AAW98079;
 DT 21-JUN-1999 (first entry)
 XX
 DE Rye chitinase-like protein CHT9 preprotein.
 XX
 KW CHT9; chitinase-like protein; antifreeze protein; AFP;
 KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
 KW transgenic plant; preservation; cryopreservation; tumour; therapy.
 XX
 OS Secale cereale.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /note= "signal peptide"
 FT Protein 21..318
 FT Protein /note= "mature protein, also claimed in Claim 10"
 XX
 PN W09906565-A2.
 XX
 XX 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-CA00745.
 XX
 PR 31-JUL-1997; 97US-0903872.
 XX
 PA (ICEB-) ICE BIOTECH INC.
 XX
 PI Griffith M, Hew C, Moffatt B, Xiong F;
 XX
 DR WPI: 1999-153795/13.
 DR N-FSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
 PT particularly with chitinase activity, used to impart frost, and
 PT pathogen, resistant to plants, for preservation of foods, cells etc.
 PT and for treating tumours
 XX
 XX Claim 10; Fig 21a; 118ps; English.

The present sequence is winter rye (Secale cereal L. cv. Muskateer)
 CC CHT9 preprotein. The mature protein, which is also claimed, is a
 CC chitinase-like protein that has chitinase (antifungal) and
 CC antifreeze activities. CHT9 cDNA (see AAX24889) was obtained by
 CC isolating mRNA from rye plants grown at low temperatures in the
 CC absence of pathogens or other stresses, i.e. under conditions when
 CC only chitinases with antifreeze activity would be expressed. CHT9
 CC and CHT46 (see AAW98081-82) have been cloned and expressed in
 CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
 CC The chitinase-like antifreeze proteins can be used: to increase
 CC freezing tolerance of plants and microorganisms; to increase field
 CC survival of plants, animals and microorganisms exposed to sub-zero
 CC temperatures; to inhibit ice recrystallisation in biological
 CC materials or foods; for cryopreservation and hypothermic protection
 CC of cells, embryos, tissues etc. (particularly human platelets); and
 CC to kill tumour cells. They are also used to inhibit initiation and
 CC progression of diseases or spoilage caused by low temperature
 CC pathogens (particularly fungi) in plants, frozen foods and any
 CC cryopreserved biological material. The signal peptide can be used
 CC to direct protein secretion in transgenic organisms or expression
 CC systems.

Sequence 318 AA;

Query Match 95.7%; Score 1688.5; DB 20; Length 318;
 Best Local Similarity 95.3%; Pred. No. 2.1e-131;
 Matches 304; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 DB 1 MRGVVVVAMLAFAVSAHAECGSGAGATCPNCLCSKFGCGTSDYCGTSCQSQCN 60
 QY 61 GCSGGTVPVPTPSGGVSSISQSLFDQMLLRNDACIAKAGFYNGAFVAAANSFSGF 120
 DB 61 GCSGGTVPVPTPSGGVSSISQSLFDQMLLRNDACIAKAGFYNGAFVAAANSFSGF 120
 QY 121 ATGSTDVKKREVAFLAQTHSHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 180
 DB 121 ATGSTDVKKREVAFLAQTHSHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 180
 QY 181 CAPGKKYFGRGPIQISHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 240
 DB 181 CAPGKKYFGRGPIQISHNYGPAQAIGTDLNNDLVASDATVSKTALWFWMTQSP 240
 QY 241 KPSSHDTVTRWSPSGADQAAGRPVGYVTNINGLGECGRGDGRVADRIGFYKRYCD 300
 DB 241 KPSSHDTVTRWSPSGADQAAGRPVGYVTNINGLGECGRGDGRVADRIGFYKRYCD 300
 QY 301 LLGVSYGDNLDYCNQRPFA 319
 DB 301 LLGVSYGDNLDYCNQRPFA 318

RESULT 3
 AAW98080
 ID AAW98080 standard; Protein; 298 AA.
 XX
 AC AAW98080;
 DT 21-JUN-1999 (first entry)
 XX
 DE Rye chitinase-like protein CHT9.
 XX
 KW CHT9; chitinase-like protein; antifreeze protein; AFP;

KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW transgenic plant; preservation; cryopreservation; tumour; therapy.
XX
OS Secale cereale.

XX WO9906565-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.

XX (ICEB-) ICE BIOTECH INC.

XX Griffith M, Hew C, Moffatt B, Xiong F;

XX WPI; 1999-153795/13.

XX N-PSDB; AAX24889.

XX New nucleic acid encoding antifreeze polypeptides from plants -
PT particularly with chitinase activity, used to impart frost, and
PT pathogen, resistant to plants, for preservation of foods, cells etc.
PT and for treating tumours
XX
PS Claim 10; Fig 21d; 118pp; English.

XX The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CC CHT9 mature protein. It lacks the 20-amino acid signal peptide
CC of the preprotein (see AAW98079), which is also claimed. Mature CHT9
CC is a chitinase-like protein that has chitinase (antifungal) and
CC antifreeze activities. CHT9 preprotein cDNA (see AAX24889) was
CC obtained by isolating mRNA from rye plants grown at low temperatures
CC in the absence of pathogens or other stresses, i.e. under conditions
CC when only chitinases with antifreeze activity would be expressed.
CC CHT9 and CHT46 (see AAW98081-82) have been cloned and expressed in
CC bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
CC The chitinase-like antifreeze proteins can be used: to increase
CC freezing tolerance of plants and microorganisms; to increase field
CC survival of plants, animals and microorganisms exposed to sub-zero
CC temperatures; to inhibit ice recrystallisation in biological
CC materials or foods; for cryopreservation and hypothermic protection
CC of cells, embryos, tissues etc. (particularly human platelets); and
CC to kill tumour cells. They are also used to inhibit initiation and
CC progression of diseases or spoilage caused by low temperature
CC pathogens (particularly fungi) in plants, frozen foods and any
CC cryopreserved biological material.

XX Sequence 298 AA;

Query Match 90.5%; Score 1597.5; DB 20; Length 298;
Best Local Similarity 95.0%; Pred. No. 6.3e-124;
Matches 284; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

QY 21 EQCGSQAGGATCPNCLCCSKFGCGTSDYCGTCQSCQNCSCSGTVPVPTPSGGVSS 80

DB 1 eqcgsgaggatcpnclccskrfgcgsteycgcgcgcqncrc-99tvpvpptpgggvss 59

QY 81 IISQSLFDQMLLRNDAACIAKAGFYNYGAFVAAANSFSGFATTGSTDYKKREVAFLAQT 140

DB 60 iisqslfdqmlhrrndaaciakagfyngafiaaansfgfattgtdvrkrevaaflaqt 119

QY 141 SHETTGGAFTAPDGPYSGWYCFNBERGATSDYCTPSSQWPCAPGKKYTGRTPIQISHN 200

DB 120 shettggaftapdgpysgwycfnbergatpssqwcpcapgkkytgrtpiqisyn 179

QY 201 YCPAGQATGTLNPNPLVADATVSKTALWFWMTPOSBPSSHDVITGWSPSGADQA 260

DB 180 ycpagratgtdlnpndlvadatvsktalwfwmtposbpsshdvltgwspsgadqa 239

QY 261 AGRVPYGVITNINGLGCGRQDGRVADRIGFYKRYCDLIGVSYGDNLCYNORPFA 319

XX

DB 240 agrvpvygvitnninglgecrgqdarvadrigfykrycdllgvsygdnlcdynqrfa 298

RESULT 4

AAR29019

ID AAR29019 standard; Protein; 336 AA.

XX AAR29019;

XX 20-APR-1993 (first entry)

XX RCH10 chitinase protein.

XX Promoter; region; rice; chitinase; physical; biological; stress;
KW leaves; stems; roots; male; female; reporter; monocotyledon;
KW dicotyledon; development; plant; defence; selectable; genes.
XX Oryza sativa.

XX Key Location/Qualifiers

XX 123..323

XX Region
FT /note= "Region conserved between class I and class
FT II chitinases"

XX WO9220807-A.

XX 26-NOV-1992.

XX 21-MAY-1992; 92WO-US04282.

XX 22-MAY-1991; 91US-0704288.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Lamb CJ, Zhu Q;

XX WPI; 1992-415785/50.

XX N-PSDB; AAO31407.

XX DNA fragment contg. chitinase gene and its regulatory region - is
PT responsive to mature plant stress and has low level expression in
PT leaves, moderate level expression in stem and high level
PT expression in roots
XX
XX Disclosure; Page 33-34; 45pp; English.

XX The sequence given is encoded by the rice chitinase gene. The promoter

XX region of this gene (see AAO31407) is responsive to physical and/or
CC biological stress. The pattern of expression of this protein in mature
CC plants is characteristic. There is a low level of expression in
CC leaves, a moderate level in plant stems and the highest level in roots
CC and the male and female parts of the plant. The chitinase promoter
CC sequence may be linked to a reporter gene for expression in mono- or
CC dicotyledon plants. Expression of this reporter gene may be used to
CC study patterns of development and controlled expression of plant
CC defence genes and selectable genes.

XX Sequence 336 AA;

Query Match 73.7%; Score 1301.5; DB 13; Length 336;
Best Local Similarity 72.3%; Pred. No. 1.8e-99;
Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVAMLAAP-AVSAHAEEQCSQAGGATCPNCLCCSKFGCGTSDYCGTGCQSQ 59

DB 1 mralavvamvparpfiaaahaeqcgsgagavcpnclccskfgwgcstdycgagcgsc 60

QY 60 N-----GCSSGTVPVPTPSGGVSSIIISQSLFDQMLLRNDAACIAKAGFYNGAFVA 112

DB 61 srlrrrrpdasgg-----ggsgvasivsrifdlmlhrrndaacpasnfytdava 112

QY 112 AANSFSGFATTGSTDYKKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNOR-GAITS 171


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QY 125 STDVKKREVAALFAQTSHETGGWPTAPDPYSWGCFNQRGATSDYCTPSSQWPCAPG 184
D 123 dldtkrevaaafgqstshettgwtapdgpfswgycfkqeggsppsycdqsadwpcapg 182
QY 185 KYFGRGPTQISHNNYNGPAGQAIGTDLNNPDLVASDATVSKTALWMTPOSXPSS 244
D 183 kqygrgpiqlthnyngpagraigvdlhnpdlvatdptvarftaiwmttqskpsc 242
QY 245 HDVITGRWSPSGADQAAGRVPYGVITNINGLGCRGQDGRVADRIGFYKRYCDLLGV 304
D 243 hdvitglwrtardsaagrvpygvitnvngiecmgmgndkvadrigfykrycdifgi 302
QY 305 SYGDNLDYCNQRPFF 318
D 303 gygnldcynqisf 316

RESULT 7
AAB67444
ID AAB67444 standard; Protein; 336 AA.
XX
AC AAB67444:
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a rice chitinase designated RCH10.
XX
KW Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase;
KW Xanthomonas; plant pathogen; Br11 protein; RCH10 protein.
XX
OS Oryza sp.
XX
PN WO200109283-A2.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-US20714.
XX
PR 28-JUL-1999; 99US-0363313.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Ronald P, He Z, Chory J, Lamb C, Li J;
XX
DR WPI; 2001-159858/16.
DR N-PSDB; AAF54983.
XX
CHimeric plant receptors comprising a polynucleotide encoding a RKK
PT receptor containing a heterologous extracellular domain and a kinase
PT domain from a Xa21 polypeptide, useful for modulating plant responses
PT to pathogens -
XX
PS Disclosure; Page 45-46; 47pp; English.
XX
CC The present sequence represents a chitinase designated RCH10. The
CC specification describes chimeric receptors which are used for modulating
CC plant responses to pathogens. The receptors comprise a heterologous
CC extracellular domain (e.g. from a Br11 protein or RCH10 protein) and
CC a kinase domain (e.g. from disease resistance protein Xa21). The Xa21
CC gene is a member of disease resistance genes referred to as RKK genes.
CC When Xa21 is present in a transgenic plant, it confers resistance to
CC Xanthomonas spp.. The plant receptors containing heterologous domains
CC are useful for modulating plant responses to pathogens including viruses,
CC bacteria, nematodes, fungi or insects. The nucleic acids can be used to
CC confer desired traits on essentially any plant.
XX
SQ Sequence 336 AA;

Query Match 73.2%; Score 1291.5; DB 22; Length 336;
Best Local Similarity 71.6%; Pred. No. 1.2e-98;
Matches 235; Conservative 27; Mismatches 49; Indels 17; Gaps 4;
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```
QY 1 MRGVVVVAMLAAP-AVSAHAECQSQAGATCPNCLCCSKFQCGTTSYDYGTCGQSQSC 59
D 1 mralavvamvarpfiaaavhaeqsgagavcpncclccsfqwcgdstdycgagcsgc 60
QY 60 N-----GCSGTPVPVTPPSGGVSSIIISQSLFDQMLLHRRNDAACLAKGFYNYGAFA 112
D 61 srllrrrrpdasgg-----ggsgvasivsrslfdmlhlhrrndaacpasnfitydafva 112
QY 113 AANSFSGFATITGTDVKREVAALFAQTSHETGGWPTAPDPYSWGCFNQRGATSD 171
D 113 aasafgfaagadadnkravaafiaqtshettggwatapdgpptwtgycfkeengagpd 172
QY 172 YCTPSSQWPCAPGKYYFGRGPTQISHNNYNGPAGQAIGTDLNNPDLVASDATVSKTAL 231
D 173 ycgqsaqwpcaagkyygrgpiqlsynfnfypgaggaigadllgpdldvasdatvsfdatf 232
QY 232 WFWMTPOSXPSSHDVITGRWSPSGADQAAGRVPYGVITNINGLGCRGQDGRVADR 291
D 233 wfwmtpqskpscnavatgqwtpsaddqragrvpygvitnlikgglecgbgeddriadr 292
QY 292 IGFYKRYCDLLGVSYGDNLDYCNQRPFA 319
D 293 igfykrycdifgvsyganldcysgrpsa 320

RESULT 8
AAR15841
ID AAR15841 standard; Protein; 329 AA.
XX
AC AAR15841:
XX
DT 19-MAR-1992 (first entry)
XX
DE Basic chitinase 48 from clone lambdaCHN17.
XX
KW Vacuole; targeting; chitinase; glucanase; signal; resistance;
KW pharmaceutical; hormones; expression; secretion; extracellular.
XX
OS Nicotiana tabacum L. c.v. Havana 425.
XX
FH Key Location/Qualifiers
FH Region 1..148
FT /label= exon1_prod.
FT Region 149..199
FT /label= exon2_prod.
FT Region 200..329
FT /label= exon3_prod.
FT Peptide 318..329
FT /label= sig_peptide
FT /note= "used as vacuole targeting peptide"
XX
PN EP462065-A.
XX
XX 18-DEC-1991.
XX
XX 06-JUN-1991; 91EP-0810430.
XX
XX 15-JUN-1990; 90CH-0002007.
XX (CIBA ) CIBA GEIGY AG.
XX
PI Boller T, Nauhaus JM, Ryals J;
XX
DR WPI; 1991-371028/51.
DR N-PSDB; AAQ15147.
XX
PT DNA sequence encoding vacuole targeting peptide - esp. signal
PT region of tobacco chitinase or glucanase gene, and derived
PT recombinant DNA, vectors, etc. functional in plants
XX
PS Disclosure; Page 64-68; 81pp; English.
XX
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PF 30-JAN-1991; 91EP-0200191.
XX
PR 30-JAN-1990; 90NL-0000222.
XX
XX (MOGE-) MOGEN INT NV.
PA (UYLE-) RIJKSUNIV TE LEIDEN.
XX
XX Cornelissen BJ, Melchers LS, Meulenhoff EJ, Van Roekel JS;
PI Sela-Buurlage MB, Vloemans AA, Woloshuk CP, Bol JF;
XX
XX WPI; 1991-232019/32.
DR N-PSDB; AAQ12898.
XX
XX Plants with improved resistance to pathogenic fungi - contains
PT chitinase and/or beta-1,3-glucanase genes modified for
PT over-expression targetted to apoplasts
XX
XX Example 4; Fig 2; 55pp; English.
XX
XX The sequence from which this amino acid was deduced was isolated
CC from a N.tobacum cDNA library following screening with a partial
CC tobacco intracellular chitinase clone. The protein sequence appears
CC twice in the specification but in one (not the one given in this
CC file), the leu codons at positions -23, -21, -15, -12, -11, -8, -7,
CC -6, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266,
CC 274, 286 are translated as Ile.
CC See AAQ12897-012900.
XX
XX Sequence 324 AA;
SQ

Query Match 70.9%; Score 1252; DB 12; Length 324;
Best Local Similarity 71.8%; Pred. No. 2.1e-95;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYCGTG-CQSQCNGCGGT 66
Db 11 silfslillsasaecqsgaggarcasgicccskfgwcgntndycpgncsqcpg--gpt 68

QY 67 PVPVTPSGGGVSSIIISQSLFDQMLLRNDACLAKGFYNYGAFVAAANSFSGFATTGST 126
Db 69 p-----pgggdligsiissmfdqmlkhrndnacqgkfyynafinaarsfpfgtsgdt 123

QY 127 DVKKREVAFLAQTSHETGGWPTADPGYSWGYCNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 tarkreiaaffaqtshtetggwatapdgyawgywlcwreqcspgdyctpsgqwpcapgrk 183

QY 187 YFGRGPIQISHNYNGPAGQAIGTDLLNPNDLVASDATYSFKTALFWMTPOSXPSSHD 246
Db 184 yfgrgpiqishnynygcgralgvdllnnpdlvatdpvisfksalwfwmtpskpschd 243

QY 247 VITGRWSPSCADQAGRPVGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 viigrwqpsadraanrlpgfvgvitnilingglecgrgtdrsvqdrigfyrriysilgvsp 303

QY 307 GDNLCYNORPF 318
Db 304 gdnldcgnqrsf 315

RESULT 11
AAW31297
ID AAW31297 standard; Protein; 324 AA.
XX
XX AC AAW31297;
XX
XX 11-MAR-1998 (first entry)
DE
DE Nicotiana sp. intracellular chitinase protein.
XX
XX Intracellular chitinase; antifungal; transgenic plant; synergism;
KW beta-1,3-glucanase gene; tobacco.
XX

```

```

OS Nicotiana sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= signal_peptide
FT Protein 24..324
FT /note= "intracellular protein"
XX
XX US5670706-A.
XX
XX 23-SEP-1997.
XX
XX 19-APR-1993; 93US-0047413.
XX
XX 29-JAN-1991; 91US-0647831.
XX
XX (MOGE-) MOGEN INT NV.
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Bol JF, Cornelissen BJ, Linthorst HJM, Melchers LS;
PI Meulenhoff EJS, Sela-buurlage MB, Van Roekel JSC;
PI Vloemans AA, Woloshuk CP;
XX
XX WPI: 1997-479536/44.
DR N-PSDB; AAT89952.
XX
XX Fungus-resistant transgenic plants - containing genes encoding
PT intracellular chitinase and beta-1,3-glucanase
PT
XX
XX Example 4; Fig 2; 42pp; English.
XX
XX This sequence represents an intracellular chitinase which is used
CC to construct a transgenic plant in a novel method to produce plants
CC resistant to fungal attack. Such transgenic plants expressing an
CC intracellular plant chitinase gene and a plant beta-1,3-glucanase gene
CC within its tissues are predicted to exhibit improved resistance to
CC pathogenic fungi. Such genes should be operably linked to promoters and
CC terminators and optionally a gene encoding a selectable or screenable
CC trait. Plants that overexpress the chitinase and glucanase genes
CC exhibit a synergistic antifungal effect.
XX
XX Sequence 324 AA;
SQ

Query Match 70.9%; Score 1252; DB 18; Length 324;
Best Local Similarity 71.8%; Pred. No. 2.1e-95;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAFAVSAHAEOCGSQAGGATCPNCLCCSKFGCGTTSYCGTG-CQSQCNGCGGT 66
Db 11 silfslillsasaecqsgaggarcasgicccskfgwcgntndycpgncsqcpg--gpt 68

QY 67 PVPVTPSGGGVSSIIISQSLFDQMLLRNDACLAKGFYNYGAFVAAANSFSGFATTGST 126
Db 69 p-----pgggdligsiissmfdqmlkhrndnacqgkfyynafinaarsfpfgtsgdt 123

QY 127 DVKKREVAFLAQTSHETGGWPTADPGYSWGYCNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 tarkreiaaffaqtshtetggwatapdgyawgywlcwreqcspgdyctpsgqwpcapgrk 183

QY 187 YFGRGPIQISHNYNGPAGQAIGTDLLNPNDLVASDATYSFKTALFWMTPOSXPSSHD 246
Db 184 yfgrgpiqishnynygcgralgvdllnnpdlvatdpvisfksalwfwmtpskpschd 243

QY 247 VITGRWSPSCADQAGRPVGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 viigrwqpsadraanrlpgfvgvitnilingglecgrgtdrsvqdrigfyrriysilgvsp 303

QY 307 GDNLCYNORPF 318
Db 304 gdnldcgnqrsf 315

RESULT 11
AAW31297
ID AAW31297 standard; Protein; 324 AA.
XX
XX AC AAW31297;
XX
XX 11-MAR-1998 (first entry)
DE
DE Nicotiana sp. intracellular chitinase protein.
XX
XX Intracellular chitinase; antifungal; transgenic plant; synergism;
KW beta-1,3-glucanase gene; tobacco.
XX

```


66	TPVPVPTSGGQVSIISQSLEFDQMLHRNDAACLAK-GFYNYGAFVAAANSFSGFATIG	121
67	gpppgpv-tggdLgvisnsmfdqmkhrnenscggkanfysynaftaarsfpdgtsg	125
125	STDVKKREVAAPLAQTSHTTGGWPTADPGYPYSWGVCYCFNOERGATSDYCTPSSQWPCAPG	184
126	dinarckreiaaafactshettgwpssadgpfawycflrerngpgdycpsssqwpcapg	185
185	KYFGRGPTQISHNHNYSPAGQAIGTDLNNPDLVASDATVSGFKALFWMTQSPKPKSS	244
186	rxfygrgpiqishnyngpcgraigvdlllnpdlvatdpvisfktaifwmtpqspkpsc	245
245	HDVITGRWSPSGADQAAGRPVCGVITNTIINGLGGCGRGDGRVADRIGFYKRYCDLLGV	304
246	hdviltgrwpsdgdsraurpfgivntlingglecgrgndurvqdrfgfyrriygilgv	305
305	SYGDNDLCYNQRPF 318	
306	spgndldcgnqrsf 319	
RESULT 14		
ID	AAR56860 standard; Protein; 329 AA.	
XX	XX	
XX	AAR56860;	
DT	17-FEB-1995 (first entry)	
XX	XX	
DE	Endochitinase precursor coding sequence.	
XX	XX	
KW	oxalic acid degradation; oxalate oxidase; selection marker;	
KW	tomato endochitinase; tobacco endochitinase; precursor;	
KW	pathogen resistance; plant cell selection.	
XX	XX	
OS	Lycopersicon esculentum.	
OS	Nicotiana tabacum.	
XX	XX	
FH	Key	Location/Qualifiers
Peptide	1..24	
FT	/label= pre-sequence	
FT	Region	25..75
FT	/label= pro-sequence	
FT	Protein	76..329
FT	/label= endochitinase	
XX	WO9413790-A.	
XX	XX	
PD	23-JUN-1994.	
XX	XX	
PF	07-DEC-1993;	93WO-FR01203.
XX	XX	
PR	07-DEC-1992;	92FR-0014721.
XX	XX	
PA	(SNEI) ELF SANOFI.	
XX	(ERAP) SOC NAT ELF AQUITAINE.	
XX	XX	
PI	Grezes-Besset B, Grison R, Pignard A, Schneider M;	
XX	XX	
DR	WPI; 1994-2117870/26.	
DR	N-PSDB; AAQ68352.	
XX	XX	
PT	Use of gene encoding oxalic acid degrading enzyme - for plant	
PT	cell selection, esp. gene coupled to gene-encoding protein	
PT	conferring pathogen resistance	
XX	XX	
PS	Disclosure; Page 34-37; 64pp; French.	
XX	XX	
CC	The sequence coding for wheat germin, a protein induced during	
CC	germination of wheat, is a preferred example of DNA coding for a	
CC	protein able to degrade oxalic acid. Such DNA can be coupled to a	
CC	sequence of interest, e.g. one coding for enzymes which confer	
CC	resistance to pathogens (esp. endochitinases). Plant calli which	

CC	have been successfully transformed by the sequences are selected
CC	by their ability to grow on oxalic acid-contg. medium. AAR56860 is
CC	a known sequence of a precursor of endochitinase; the sequence was
CC	previously disclosed in W09201792.
XX	
XX	
SQ	Sequence 329 AA;
Query Match	68.1%; Score 1202.5; DB 15; Length 329;
Best Local Similarity	67.8%; Pred. NO. 2.6e-91;
Matches 213; Conservative 38; Mismatches 52; Indels 11; Gaps	
QY	7 VAMLAFAFVSAHAECGSGAGGATPCNCLCCSKFGFCGTSDYCGTG-CQSOCNGCSGG 65
DB	16 lvllisaal-----aqcsggggkvcasggccskfgwcntndhocsgncsq---cpvg 67
QY	66 TPVPVPTPSGGGVSSIISLSLPDQMLHRNDAAKLAK-GFYNYGAFFVAANSPSGPATTG 124
DB	68 gpgpgpv-tggdlgsvisnsmfdqmlkhrrnenscqgknfnfysynaftaarsfpgfgtsg 126
QY	125 STDVKKREVAFAIAQTSHETWTGGTPADGPYSWGYCFNCERGATSDYCTPSSOWPCAPG 184
DB	127 dlnarkreiafaagtshettgwpapdgpfawgycfirergnpgdycpsssqwpcapg 186
QY	185 KKYEGRGPIQISHNNYGPAGCAIGTOLLNPNDLVASDATVSFKTALWFMTQPSPKPS 244
DB	187 rkyfgrpiqishnnypgcraigvdlldnpdilatcdpvisfktaifwmtpgspkpsc 246
QY	245 HDVTTRWSRSGADQAAGRVPVGIVTNINGGLECRGDGRVADRIGFYKRYCDLLGV 304
DB	247 hdvligrwnpsagdsranripfgfvitniingglecgrgndrvqdrgifryrcgilgv 306
QY	305 SYGDNLDGCYNORPF 318
DB	307 spgdnlcdcgnrfsf 320
RESULT 15	
AAW00186	
ID	AAW00186 standard; Protein; 317 AA.
AC	AAW00186;
XX	
DT	18-OCT-1996 (first entry)
DE	American elm chitinase-like protein.
KW	Clone PHS2; chitinase; american elm; fungus; Ophiostoma ulmi;
KW	dutch elm disease; E. coli; chitinase-like protein;
KW	fungal infection.
OS	American elm.
FH	Key Location/Qualifiers
FT	Peptide 1..21
FT	/note= "signal peptide"
FT	Protein 22..317
FT	/note= "Mature chitinase-like protein"
XX	
PN	US5539095-A.
PD	23-JUL-1996.
XX	
PF	04-AUG-1994; 94US-0286020.
XX	
PR	04-AUG-1994; 94US-0286020.
XX	
PA	(UNMS) UNIV MICHIGAN STATE.
XX	
PI	Hajela RK, Sticklen MB;
DR	WPI; 1996-353879/35.
N-PSTB:	AAT33325.

XX Isolated chitinase gene derived from an American elm - used to
PT obtain prods. for inhibiting fungal infection of plants
XX
PS Claim 1; Fig 1; 12pp; English.
XX
CC This sequence is encoded by the cDNA clone pHS2, and represents a protein
CC having chitinase-activity derived from American elm. This protein
CC inhibits the fungus Ophiostoma ulmi, the causative agent of dutch
CC elm disease. The clone pHS2 may be used to transform E. coli cells
CC for the recombinant production of the chitinase-like protein. The
CC protein may be used in a composition to inhibit fungal infection of
CC elm trees.
XX
SQ Sequence 317 AA;

Query Match 67.6%; Score 1192.5; DB 17; Length 317;
Best Local Similarity 70.6%; Pred. No. 1.7e-90;
Matches 211; Conservative 30; Mismatches 47; Indels 11; Gaps 3;

QY 20 AEQCGSQAGGATCPNCLCCSKGFCGTTSDYCGTGCQSCGCGSGGTPVPVPTSGGGVS 79
Db 21 aeqcgsgaggavepvglccskfgwcgstneycgdgqgcgg-sgsddi-----gg-- 70

QY 80 SIISQSLFDQMLLHRNDACIAKGFYNYGAFVAAANSFSGFATGTGTDVKKREVAFLAQ 139
Db 71 -lissafndmlkhrndggcpakfytydafiaaakafafgstgddtrkrelaafiq 129

QY 140 TSHETTGWPTAPDGPYSGYCWGCFNQRGATSDYCTPSSQWPCAPGKKYFGRGPIQISHNY 199
Db 130 tshettgwasapdgpyswgycreqnpssdycsfptwpcasgkryfgrgpiqlswny 189

QY 200 NYGPAGQAIGTDLLNPDLVASDATVSKTALFWMTPOQPKSSHVDVITGRWSPSGADQ 259
Db 190 nygcgraignanlnonpdlvatdpvisfktalwfmtpqpkpschavitgrwspsgtdq 249

QY 260 AAGRVPYGVITNINGLGECRGQDGRVADRIGFYKRYCDLLGVSYGDNLDYCNQRPF 318
Db 250 sagrvagvyvtniingiecgkgqvqvdrigfykrycdilrvygnnldcynqrpf 308

Search completed: May 3, 2002, 18:30:32
Job time: 7551 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:43:04 ; Search time 79.44 Seconds
(without alignments)
90.364 Million cell updates/sec

Title: US-09-534-229C-3

Perfect score: 1765

Sequence: 1 MRGVVVVAMLAFAFVSAHA.....DLGVSVDNLCYNORPFA 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents: AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301.5	73.7	336	1	US-07-704-288C-3
2	1301.5	73.7	336	1	US-08-093-372-2
3	1301.5	73.7	336	1	US-08-379-259-3
4	1257	71.2	310	4	US-07-791-931-6
5	1252	70.9	324	1	US-08-047-413-11
6	1252	70.9	324	3	US-08-229-050-11
7	1252	70.9	324	3	US-08-801-563-11
8	1246.5	70.6	310	1	US-07-704-288C-6
9	1246.5	70.6	310	1	US-08-379-259-6
10	1208	68.4	328	4	US-07-791-931-5
11	1202.5	68.1	329	2	US-08-475-427-13
12	1202.5	68.1	329	2	US-07-842-165-13
13	1202	68.1	330	1	US-07-704-288C-8
14	1202	68.1	330	1	US-08-379-259-8
15	1183	67.0	328	4	US-07-791-931-7
16	1175	66.6	314	1	US-07-704-288C-7
17	1175	66.6	314	1	US-08-379-259-7
18	1174.5	66.5	318	1	US-07-704-288C-9
19	1174.5	66.5	318	1	US-08-379-259-9
20	1131.5	64.1	302	2	US-08-475-427-6
21	1131.5	64.1	302	2	US-07-842-165-6
22	1125	63.7	266	1	US-08-812-025-10
23	1125	63.7	266	4	US-07-791-931-10
24	1125	63.7	266	4	US-09-138-873A-10
25	1038.5	58.8	254	2	US-08-475-427-1
26	1038.5	58.8	254	2	US-07-842-165-1
27	1038.5	58.8	254	4	US-08-448-398-3

28 805.5 45.6 254 1 US-08-047-413-9 Sequence 9, Appli
29 805.5 45.6 254 3 US-08-229-050-9 Sequence 9, Appli
30 805.5 45.6 254 3 US-08-801-563-9 Sequence 9, Appli
31 803.5 45.5 316 4 US-07-791-931-8 Sequence 8, Appli
32 777.5 44.1 253 1 US-08-162-475A-5 Sequence 5, Appli
33 763.5 43.3 253 4 US-07-791-931-9 Sequence 9, Appli
34 722.5 40.9 372 1 US-07-791-931-4 Sequence 4, Appli
35 712.5 40.4 253 1 US-08-162-475A-2 Sequence 2, Appli
36 710.5 40.3 250 1 US-08-162-475A-4 Sequence 4, Appli
37 539 30.5 130 3 US-08-329-799-37 Sequence 37, Appli
38 483.5 27.4 148 3 US-08-329-799-35 Sequence 35, Appli
39 266.5 15.1 71 1 US-07-704-288C-15 Sequence 15, Appli
40 266.5 15.1 71 1 US-08-379-259-15 Sequence 15, Appli
41 259 14.7 51 3 US-08-329-799-36 Sequence 36, Appli
42 231.5 13.1 63 1 US-07-704-288C-14 Sequence 14, Appli
43 231.5 13.1 63 1 US-08-379-259-14 Sequence 14, Appli
44 187 10.6 41 1 US-08-149-839B-9 Sequence 9, Appli
45 187 10.6 41 1 US-08-451-568-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-3
; Sequence 3, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-704-288C-3

Query Match 73.7%; Score 1301.5; DB 1; Length 336;

Best Local Similarity 72.3%; Pred. No. 5.8e-111;

Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVAMLAFAFVSAHAECGSGAGATCPNCLCCSKFQGTTSYCGTGCGSQSC 59

|| : ||||| : || : ||||| : || : ||||| : || : ||||| : || : ||||| : |||||

Db 1 MRALAVVMVAVRFLAAAVHAECGSGAGAVCPNCLCCSQFGWCGSTSDYCGAGCGSQSC 60

QY 1 MRGVVVVLAALAAAF-AVSAHAEOCGSAGGATCPNCLCCSKFGCGTTSYCYGTCGQSQC 59
Db 1 MRALAVVAVARFLAAVARECCSAGAGVAPCNCLCCSFGCGSTSYCYGTCGQSQC 60
QY 60 N-----GCSGGTTPVPPTPSGGGVSSIIQSQSLDFQMLLHRNDAACLAKGFYNYGAFVA 112
Db 61 SRLRRRPDASGG-----GGSGVASIVSRSLDFMLLHRNDAACPASNFYTYDAFVA 112
QY 113 AANSFSGFATGTSDVKKREVAALFAOTSHTTGGWTPADPGPYSGWYCFNQER-GATSD 171
Db 113 AASAFPFGAAGDADTNKREVAALFAOTSHTTGGWATAPDGPYTWGCFKRENGGAGPD 172
QY 172 YCTPSSQWPCAPGKKYGRGPIQIOTSHNNYGPAGOAIGTDLNNPDLVASDATVSFKTAL 231
Db 173 YCQSAQWPCAPGKKYGRGPIQIOLSYNNYGPAGOAIGADLLGDPDLVASDATVSFDTAF 232
QY 232 WFWMTQSPKPSHDVITGRWSGSAQAAGRVPGYGVITNINGLGECGQDGRVADR 291
Db 233 WFWMTQSPKPCNAVATGOWTPSADQORAGRVPGYGVITNINGLGECGHGDDRIADR 292
QY 292 IGFYKRYCDLLGVSGYGNLDCYNORPFA 319
Db 293 IGFYKRYCDLLGVSYGNALDCYSORPSA 320

RESULT 4

US-07-791-931-6
; Sequence 6, Application US/07791931C
; Patent No. 6133567
; GENERAL INFORMATION:
; APPLICANT: RaiXhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-07-791-931-6

Query Match 71.2%; Score 1257; DB 4; Length 310;
Best Local Similarity 73.7%; Pred. No. 5.9e-107;
Matches 224; Conservative 26; Mismatches 46; Indels 8; Gaps 3;

QY 15 VSAHAEOCGSAGGATCPNCLCCSKFGCGTTSYCYGTCG-CQSQNGCGSGTTPVPPTPS 74
Db 5 LSASAEQCGSAGGATCPNCLCCSKFGCGTNDYCGPGNCGSQCPG--GPTP-----PG 57
QY 75 GGGVSSIIQSLSLDFQMLLHRNDAACLAKGFYNYGAFVAANFSFGFATTGSDVKKREVA 134
Db 58 GDLGSLIISSSDFQMLKRNNDACQKGFYSYNAPFINAARFPFGTSGDITARKRETA 117
QY 135 AFLAOTSHTTGGWTPADPGPYSGWYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
Db 118 AFAAOTSHTTGGWATAPDGPYAWGYCWLREOGSPGDCYCTPSSQWPCAPGKKYFGRGPIQ 177
QY 195 ISHNNYGPAGOAIGADLLNNPDLVASDATVSFKTALWFWMTQSPKPSHDVITGRWSP 254
Db 178 ISHNNYGPAGOAIGADLLNNPDLVASDATVSFKTALWFWMTQSPKPSHDVITGRWOP 237
QY 255 SGADQAAGRVPGYGVITNINGLGECRGDGRVADRIGFYKRYCDLLGVSYGNLDCYN 314
Db 238 SSADRANRLPGVGIVITNINGLGECRGDGRVADRIGFYKRYCDLLGVSYGNLDCGN 297
QY 315 QRPF 318
Db 298 QRSF 301

RESULT 5
US-08-047-413-11
; Sequence 11, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Fester
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/047,413
; FILING DATE: 19-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-047-413-11

Query Match 70.9%; Score 1252; DB 1; Length 324;

Best Local Similarity 71.8%; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAAFVSAHAEOCGSAGGATCPNCLCCSKFGCGTTSYCYGTCG-CQSQNGCGSGT 66
Db 11 SLILSLLLSASAEQCGSAGGATCPNCLCCSKFGCGTNDYCGPGNCGSQCPG--GPT 68
QY 67 PVPPTPSGGGVSSIIQSLSLDFQMLLHRNDAACLAKGFYNYGAFVAANFSFGFATTG 126
Db 69 P-----PGGDLGSLIISSSDFQMLKRNNDACQKGFYSYNAPFINAARFPFGTSG 123
QY 127 DVKKREVAALFAOTSHTTGGWTPADPGPYSGWYCFNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 TARKREIAFAAOTSHTTGGWATAPDGPYAWGYCWLREOGSPGDCYCTPSSQWPCAPGKK 183
QY 187 YFGRGPIQIOTSHNNYGPAGOAIGADLLNNPDLVASDATVSFKTALWFWMTQSPKPSHD 246
Db 184 YFGRGPIQIOTSHNNYGPAGOAIGADLLNNPDLVASDATVSFKTALWFWMTQSPKPSHD 243

QY 247 VTGRWPSGADQAAGRVPGYGVITNINLINGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VTIGRWQPSADRAANRLPFGVITNINLINGLECGRGTDSDRVQDRIGFYRRYCSILGVSP 303
QY 307 GDNLCYNQRPF 318
Db 304 GDNLCGNQRSF 315

RESULT 6
US-08-229-050-11
; Sequence 11, Application US/08229050
; Patent No. 6066491
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-229-050-11

Query Match 70.9%; Score 1252; DB 3; Length 324;
Best Local Similarity 71.8%; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;

QY 8 AMLAAAFVASHARCCSQAGGATCPNCLCCSKFGFCGTSDYCGTG-CQSQCNCGSGGT 66
Db 11 SLFLSLLLSASRQCQSGAGRCASLCCSKFGCGGNTNDYCGPGNCGQCPG--GPT 68
QY 67 PVPYPTSGGGVSSISQSLFDQMLLHNDAACLAAGFYNGAFVAAANSFGFATIGST 126

Db 69 P-----PGGDLGSLISSSMFDQMLKHRNDNACQKGFYSYNAFINAARSFPGFGTSGDT 123
QY 127 DVKKREVAFLAQTSHTTGGTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
Db 124 TARKREIAAFFAQTSHTTGGTAPDGPYAWGYCWLREQCSPGDYCTPSGOWPCAPGKK 183
QY 187 YFGRGPQIQISHNYNYPGAGQATGTDLLNPNPLVASDATVSEKTALEWFWMTQSPKPSHD 246
Db 184 YFGRGPQIQISHNYNYPGCGAIGVDLLNPNPLVATDPISEKALWFWMTQSPKPSCHD 243
QY 247 VTGRWPSGADQAAGRVPGYGVITNINLINGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VTIGRWQPSADRAANRLPFGVITNINLINGLECGRGTDSDRVQDRIGFYRRYCSILGVSP 303
QY 307 GDNLCYNQRPF 318
Db 304 GDNLCGNQRSF 315

RESULT 7
US-08-801-563-11
; Sequence 11, Application US/08801563
; Patent No. 6087560
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Sela-Buurlage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,563
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,413
; FILING DATE: 19-APR-1993
; APPLICATION NUMBER: US 07/647,831
; FILING DATE: 29-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20022.00
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-801-563-11

Query Match 70.98; Score 1252; DB 3; Length 324;
Best Local Similarity 71.88; Pred. No. 1.8e-106;
Matches 224; Conservative 29; Mismatches 51; Indels 8; Gaps 3;
QY 8 AMLAAFAVSAHAECQAGAGATPCNLCCKFGCGTTSYCGTG-CQSCQNCSCSGT 56
Db 11 SLLSLLLSASAQCQAGAGARACGLCCSKFGWCGTNDYCGPGNQSQCPG--GPT 68
QY 67 PVPVPTGGVSSIIISQSLFDQMLLRNDAACLAAGFYNYGAFVAAANSFGFATTG 126
Db 69 P-----PGGDLGSISSSMEDQMLKRNDAACQCKGFGYSYNAFTNAARSPFGTSGDT 123
QY 127 DVKKREAAFAAOTSHETGGWPTAPDGPYSGYCFNCRGATSDYCPSSQWPCAPGKK 186
Db 124 TARKREIAFAAOTSHETGGWPTAPDGPYSGYCFNCRGATSDYCPSSQWPCAPGKK 183
QY 187 YFGRPIQISHNYNGPAGQATGTDLLNPDIVASDATVSKTALFWFMTQSPKPS 246
Db 184 YFGRPIQISHNYNGPAGQATGTDLLNPDIVASDATVSKTALFWFMTQSPKPS 243
QY 247 VITGKSSGDAQAGRVPGYGVITNIIINGLCCGGRGQVADRGIGFYKRYCDLLGYSY 306
Db 244 VITGKSSGDAQAGRVPGYGVITNIIINGLCCGGRGQVADRGIGFYKRYCDLLGYSY 303
QY 307 GDNLDYCNORPF 318
Db 304 GDNLDYCNORSF 315

RESULT 8
US-07-704-288C-6
; Sequence 6, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: DEFENSE ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-07-704-288C-6

Query Match 70.6%; Score 1246.5; DB 1; Length 310;
Best Local Similarity 73.7%; Pred. No. 5.4e-106;
Matches 224; Conservative 26; Mismatches 45; Indels 9; Gaps 4;
QY 16 VSAHAECQAGAGATPCNLCCKFGCGTTSYCGTG-CQSCQNCSCSGTQSPKPS 74
Db 6 LSAAECQAGAGARACGLCCSKFGWCGTNDYCGPGNQSQCPG--GPT-----PG 58
QY 75 GGVSSIIISQSLFDQMLLRNDAACLAAGFYNYGAFVAAANSFGFATTGDKKREVA 134
Db 59 GGDGSISSSMEDQMLKRNDAACQCKGFGYSYNAFTNAARSPFGTSGDTTARKREIA 118
QY 135 AFLAQTSHETGGWPTAPDGPYSGYCFNCRGATSDYCPSSQWPCAPGKKYFGRGPIQ 194
Db 119 AFFAQTSHETGGWPTAPDGPYSGYCFNCRGATSDYCPSSQWPCAPGKKYFGRGPIQ 178
QY 195 ISHNTYNGPAGQATGTDLLNPDIVASDATVSKTALFWFMTQSPKPS 254
Db 179 ISHNTYNGPAGQATGTDLLNPDIVASDATVSKTALFWFMTQSPKPS 237
QY 255 SGADQAGRVPGYGVITNIIINGLCCGGRGQVADRGIGFYKRYCDLLGYSY 314
Db 238 SSADRAANRLPGYGVITNIIINGLCCGGRGQVADRGIGFYKRYCDLLGYSY 297
QY 315 QRPF 318
Db 298 QRSF 301

RESULT 9
US-08-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids

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; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-6

Query Match          70.6%; Score 1246.5; DB 1; Length 310;
Best Local Similarity 73.7%; Pred. No. 5.4e-106;
Matches 224; Conservative 26; Mismatches 45; Indels 9; Gaps 4;

QY 16 VSAHQCGSQAGGATCPNCLCCSKFGCGTTSYDYGCGTG-CQSQCNGCSGGIPVVPVPTFS 74
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 6 LSASAEQCGSQAGGATCPNCLCCSKFGCGTNDYCGPGNCQSQCPG--GPTP-----PG 58

QY 75 GGVVSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATGTGSTDVKKREVA 134
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 59 GGDLSIISSMFDQMLKHRNDACQKGFYSYNAFINARSFPGTSGDITFARKREIA 118

QY 135 AFLAQTSHETTGWPTAPDGPYSWGCFNQRGATSDYCTPSSQWPCAPGKGYFGRGPIQ 194
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 119 APTAQTSHETTGWATPDGPYANGYCWLEQSGPDYCTPSSQWPCAPGKGYFGRGPIQ 178

QY 195 ISHNYNGPAGQAGIDLLNPNPDLVADATVSKTALFWMTPOSKPSPSHDVTGRWSP 254
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 179 ISHNYNGPGRGAIQVLDLLNPNPDLVATDPVISEKSALEWMTPOSKPSPCHDVIIGRW-P 237

QY 255 SGADQAGRPVPGYGVITNIINGLECGRGODGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 238 SSADRAANRLPGFVITNIINGLECGRGDTSRVQDRIGFIRYKYSILGVSQDNLDCGN 297

QY 315 QRPFP 318
   :|||
Db 298 QRSF 301

RESULT 10
US-07-791-931-5
; Sequence 5, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-07-791-931-5

Query Match          58.4%; Score 1208; DB 4; Length 328;
Best Local Similarity 59.0%; Pred. No. 1.9e-102;
Matches 218; Conservative 31; Mismatches 57; Indels 10; Gaps 4;

QY 7 VAMLAFAFV---SAHAEOCSQAGGATCPNCLCCSKFGCGTTSYDYGCGTG-CQSQCNGC 62
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 10 VAYLLFSLVLSAALQNCQSGGGKACASGQCCKFGWCNCTNDYCGSGNCQSQ---C 66

QY 63 SGGTPVPVPTSGGGVSSIIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 67 PGGPGPGP---GGDLGSAISNMFQDMLKHRNENSCQKGFYSYNAFINARSFPGT 123

QY 123 TGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGCFNQRGATSDYCTPSSQWPCA 182
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 124 SGGDINARKREIAFAAQTSHETTGWASAPDGPYAWGYCFILRGNPGDGYCPPSSQWPCA 183

QY 183 PGKRYFGRGPIQISHNYNGPAGQAGIDLLNPNPDLVADATVSKTALFWMTPOSKP 242
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
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Db 10 VAYLLFSLVLSAALQNGSGGGKACASQCCSKFGWCGTNDYCGSGNCQSQ---C 66
QY 63 SGGTVPVPTSSGGVSSIIISQSLFDQMLLHRNDAAKAGFYNYGAFVAANSSGFGAT 122
Db 67 PGGGPGPGP---GGDLGSAISNMFQMLKHNENSCOGKFNFSYNAFINAAARSPPGFGT 123
QY 123 TGSTDVKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNCRGATSDYCTPSSQWPCA 182
Db 124 SGIINARKREIAAFAQTSHETTTGGWASAPDGPYAWGYCFNCRGATSDYCTPSSQWPCA 183
QY 183 PGKVFGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 242
Db 184 PGKVFGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 243
QY 243 SSHDVTGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 302
Db 244 SCDVITGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 303
QY 303 GVSYGNDLDCYNORPF 318
Db 304 GVTPGNDLDCYNORWF 319

RESULT 14

US-08-379-259-8
; Sequence 8, Application US/08379259
; Patent No. 5695939
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
; TITLE OF INVENTION: DEFENSE REGULATORY
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,259
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 07/704,288
; FILING DATE: 22-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-8

Query Match 68.1%; Score 1202; DB 1; Length 330;
Best Local Similarity 68.7%; Pred. No. 6.6e-102;

Matches 217; Conservative 31; Mismatches 58; Indels 10; Gaps 4;
QY 7 VAMLAFAFAV---SAFAEQCSQAGSATPCNLCCKSKFGCGTTSDYCGTG-CQSQCNCG 62
Db 10 VAYLLFSLVLSAALQNGSGGGKACASQCCSKFGWCGTNDYCGSGNCQSQ---C 66
QY 63 SGGTVPVPTSSGGVSSIIISQSLFDQMLLHRNDAAKAGFYNYGAFVAANSSGFGAT 122
Db 67 PGGGPGPGP---GGDLGSAISNMFQMLKHNENSCOGKFNFSYNAFINAAARSPPGFGT 123
QY 123 TGSTDVKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNCRGATSDYCTPSSQWPCA 182
Db 124 SGIINARKREIAAFAQTSHETTTGGWASAPDGPYAWGYCFNCRGATSDYCTPSSQWPCA 183
QY 183 PGKVFGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 242
Db 184 PGKVFGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 243
QY 243 SSHDVTGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 302
Db 244 SCDVITGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 303
QY 303 GVSYGNDLDCYNORPF 318
Db 304 GVTPGNDLDCYNORWF 319

RESULT 15

US-07-791-931-7
; Sequence 7, Application US/07791931C
; Patent No. 6133507
; GENERAL INFORMATION:
; APPLICANT: Raikhel, Natasha V.
; TITLE OF INVENTION: Nettle Lectin cDNA
; FILE REFERENCE: MSU 4.1-114
; CURRENT APPLICATION NUMBER: US/07/791,931C
; CURRENT FILING DATE: 1991-11-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Phaseolus vulgaris
US-07-791-931-7

Query Match 67.0%; Score 1183; DB 4; Length 328;

Best Local Similarity 67.1%; Pred. No. 3.5e-100;

Matches 212; Conservative 36; Mismatches 54; Indels 14; Gaps 4;

QY 3 GVVVAMLAFAFAVSAFAEQCSQAGSATPCNLCCKSKFGCGTTSDYCGTGCGSQCNCG 62
Db 14 GVVVAMLLLVG---GSYGECQAGGALCPGGNCCSQFGWCGSTTDYCGPCCQCGG- 68
QY 63 SGGTVPVPTSSGGVSSIIISQSLFDQMLLHRNDAAKAGFYNYGAFVAANSSGFGAT 122
Db 69 ----PSAPTI----DISALISRTFDQMLKHNDCACPAKGYTYDAFTAAAKAYPSFGN 120
QY 123 TGSTDVKKREVAALFAQTSHETTTGGWPTAPDGPYSGWYCFNCRGATSDYCTPSSQWPCA 182
Db 121 TGDATRKREIAAFLGQTSHTTGGWATAPDGPYAWGYCFVBERN-PSYCSATPQPPCA 179
QY 183 PGKVFGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 242
Db 180 PGQVITGRGPIQISHNINYPGAGQAGTIDLLNPNPLVADATVSKTALFWFMTPOSQPKP 239
QY 243 SSHDVTGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 302
Db 240 SSHDVTGRWSPGADQAGRPVGYVTIININGLECGRGODGRVADRIGFYKRYCDDL 299
QY 303 GVSYGNDLDCYNORPF 318
Db 300 GVGYNLDCYSQITPF 315

Search completed: May 3, 2002, 18:43:05
Job time: 748 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:32:12 ; Search time 88.01 Seconds
(without alignments)
276.101 Million cell updates/sec

Title: US-09-534-229C-3
Perfect score: 1765
Sequence: 1 MRGVVVVAMLAFAVSAHA.....DLLGVSYGDNLDYQNRPFA 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

30	1168.5	66.2	327	1	JQ0965	chitinase (EC 3.2.
31	1167.5	66.1	329	2	T06999	chitinase (EC 3.2.
32	1162	65.8	321	2	S57482	chitinase class 1
33	1156	65.5	308	2	JC2253	chitinase (EC 3.2.
34	1154.5	65.4	302	2	T10810	chitinase (EC 3.2.
35	1140	64.6	243	2	JN0884	chitinase (EC 3.2.
36	1125	63.7	266	2	A38664	chitinase (EC 3.2.
37	1120	63.5	243	2	JC5918	chitinase (EC 3.2.
38	1099.5	62.3	318	2	T03026	chitinase (EC 3.2.
39	1071	60.7	263	2	S72528	chitinase (EC 3.2.
40	1045	59.2	264	2	S26625	chitinase (EC 3.2.
41	1022.5	57.9	340	2	S48030	probable chitinase
42	1012	57.3	263	2	S69184	chitinase (EC 3.2.
43	1004	56.9	246	2	S37341	chitinase (EC 3.2.
44	993	56.3	336	1	S18750	chitinase (EC 3.2.
45	966	54.7	275	2	T03032	chitinase (EC 3.2.

ALIGNMENTS

RESULT 1
S38670
chitinase (EC 3.2.1.14) - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
C:Accession: S38670
R:Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener, H.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38670
A:Accession: S38670
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <LIA>
A:Cross-references: EMBL:X76041; NID:g416028; PID:CAA53626.1; PID:g416029
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-320/Domain: plant chitinase homology <PCH>

Query Match	96.1%	Score 1696.5;	DB 2;	Length 320;
Best Local Similarity	95.3%	Pred. No. 6.8e-119;		
Matches	305;	Conservative	9;	Mismatches 5; Indels 1; Gaps 1;

Qy	1	MRGVVVVAMLAFAVSAHAECQCGSQAGGATCPNCLCCSKFEGCGTTSQDYCGTGCGSQCN	60
Db	1	MRGVVVVAMLAFAVSAHAECQCGSQAGGATCPNCLCCSKFEGCGTTSQDYCGTGCGSQCN	60
Qy	61	GCS-GGTPVPVPTPGSGGVSSIIQSLSFDQMLLHRNDAACLAKEFYNYGAFVAAANSFSG	119
Db	61	GCSGGGTPVPVPTPGSGGVSSIIQSLSFDQMLLHRNDAACQAKGFYNYGAFVAAANSFSG	120
Qy	120	FATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNQERGATSDYCTPSSQW	179
Db	121	FATTGGADVRRKREVAFLAQTSHETTGWPTAPDGPYSGWYCFNQERGAASDYCPNSQW	180
Qy	180	PCAPGKKYFGRGPIQISHNYNYPGAGQAGTDPDLNPNLVDASDATVSPKTALEWMTPOS	239
Db	181	PCAPGKKYFGRGPIQISHNYNYPGAGRAIGTDLNPNLVDATVSPKTALEWMTPOS	240
Qy	240	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLEGGRGDGRVADRIGFYKRYC	299
Db	241	PKPSSHVDITGRWSPSGADQAAGRVPGYGVITNIINGLEGGRGDGRVADRIGFYKRYC	300
Qy	300	DLLGVSYGDNLDYQNRPFA	319
Db	301	DLLGVSYGDNLDYQNRPFA	320

RESULT 2
JC2071
chitinase (EC 3.2.1.14) a - rye

Tue May 7 10:52:26 2002

C:Species: Secale cereale (rye)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C:Accession: JC2071
R:Yamagami, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 58, 322-329, 1994
A:Title: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale cereale L.)
A:Reference number: JC2071; MUID:94169514
A:Accession: JC2071
A:Molecule type: protein
A:Residues: 1-302 <VAM>
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-42/Domain: hevein chitin-binding domain homology <HCB>
F:64-302/Domain: plant chitinase homology <PCH>

Query Match 80.3%; Score 1416.5; DB 2; Length 302;
Best Local Similarity 82.1%; Pred. No. 4e-98;
Matches 248; Conservative 26; Mismatches 25; Indels 3; Gaps 3;
QY 21 EQCGSQAGGATPCNCLCCSKFPGCGTSDYCGTGCQSQNGC-SGGTPV-PVPTPS-GGG 77
Db 1 EQCGSQAGGATPCNCLCCSKFPGCGTSDYCGTGCQSQNGC-SGGTPV-PVPTPS-GGG 60
QY 78 VSSIISQSLFDQMLLHRNDACLAAGFYNYGAFVAAANSPFGATGTDVKKREVAFL 137
Db 61 VSSIISQSLFDQMLLHRNDACLAAGFYNYGAFVAAANSPFGATGTDVKKREVAFL 120
QY 138 AQTSHETGGWPTAPDGPYSGWYCFNBERGATSDYCPSSOWPCAPGKFFGRGPIQLSH 197
Db 121 AQTSHETGGWATAPDGAFAWGYCFKBERGATSNYCTPSAOWPCAPGKSYGRGPIQLSH 180
QY 198 NNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOSPPSHDVTGTRWSPSGA 257
Db 181 NNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOSPPSHDVTGTRWSPSGT 240
QY 258 DOAAGRPVGVYNTNIINGLEGCGRQDGRVADRIGFYKRYCDLILGVSYGNLDCYNORP 317
Db 241 DRAGRPVGFYNTNIINGLEGCGRQDGRVADRIGFYKRYCDLILGVSYGNLDCYNORP 300
QY 318 FA 319
Db 301 FA 302

RESULT 3
T04403
probable chitinase (EC 3.2.1.14) precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
C:Accession: T04403
R:Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
submitted to the EMBL Data Library, September 1993
A:Description: Isolation and characterization of a barley chitinase genomic clone.
A:Reference number: Z15336
A:Accession: T04403
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-318 <IGN>
A:Cross-references: EMBL:U02287; NID:g495304; PID:AAA18586.1; PID:g495305
A:Experimental source: cv. NK1556
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; plant chitinase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-318/Product: chitinase #status predicted <MAT>
F:20-60/Domain: hevein chitin-binding domain homology <HCB>
F:80-318/Domain: plant chitinase homology <PCH>

Query Match 79.7%; Score 1407.5; DB 2; Length 318;
Best Local Similarity 77.8%; Pred. No. 2e-97;
Matches 249; Conservative 33; Mismatches 35; Indels 3; Gaps 3;

QY 1 MRGVVVVAMLAFAVAFAHAECQSQAGATPCNCLCCSKFPGCGTSDYCGTGCQSQCN 60
Db 1 MRAFLVFAVMA-ATMAVAECQSQAGATPCNCLCCSKFPGCGST-PYCGDGCQSQCS 58
QY 61 GCGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDACLAAGFYNYGAFVAAANSPFG 119
Db 59 GCGGTPVPVPTPSGGGGVSSIISQSLFDQMLLHRNDACLAAGFYNYGAFVAAANSPFG 118
QY 120 FATGSTDVKKREVAFLAQTSHETGGWPTAPDGPYSGWYCFNBERGATSDYCTPSSOW 179
Db 119 FGTGTDTRKREVAFLAQTSHETGGWATAPDGAFAWGYCFKBERGATSNYCTPSAOW 178
QY 180 PCAPGKFFGRGPIQLSHNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOS 239
Db 179 PCAPGKSYGRGPIQLSHNYGPAQAGTDLNNPDLVSDATVSEKTLFWMTPOS 238
QY 240 PKSSHVDVTGRWSPSGADQAGRPVGVYNTNIINGLEGCGRQDGRVADRIGFYKRYC 299
Db 239 PKSSHAVITGQWSPSGTDRAGRPVGFYNTNIINGLEGCGRQDGRVADRIGFYKRYC 298
QY 300 DLLGVSYGNLDCYNORPFA 319
Db 299 DILGVSYGNLDCYSORPFA 318
RESULT 4
T03614
chitinase (EC 3.2.1.14) - rice
N:Alternate names: endochitinase
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03614
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice
A:Reference number: S39979; MUID:94049667
A:Accession: T03614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-323 <NIS>
A:Cross-references: EMBL:D16221; NID:g452232; PIDN:BA03749.1; PID:g500615
A:Experimental source: cv. Nipponbare
C:Genetics:
A:Gene: Cht-1
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase
F:21-62/Domain: hevein chitin-binding domain homology <HCB>
F:82-322/Domain: plant chitinase homology <PCH>

Query Match 77.0%; Score 1359.5; DB 2; Length 323;
Best Local Similarity 75.6%; Pred. No. 7.3e-94;
Matches 245; Conservative 27; Mismatches 43; Indels 9; Gaps 4;
QY 1 MRGVVVVAMLAFAVAFAHAECQSQAGATPCNCLCCSKFPGCGTSDYCGTGCQSQCN 60
Db 1 MRALAVVVATAFVAVVVRGCGSQAGGALCPNCLCCSKYGCWGSTSYCGSQSQCS 60
QY 61 G-CSGTFPVPTPSGG---GVSSIISQSLFDQMLLHRNDACLAAGFYNYGAFVAAAN 116
Db 61 GSGCGGTPP---PSGCGGSGVASYVRSFLDQMLLHRNDACPAKNFTYDAFVAAANA 117
QY 117 FSGFATGSTDVKKREVAFLAQTSHETGGWPTAPDGPYSGWYCFNBERGAT--SDYCT 174
Db 118 FSGFATGDAATRKREVAFLAQTSHETGGWATAPDGPYSGWYCFKBERGATVDF 177
QY 175 PSSQWPCAPGKFFGRGPIQLSHNYGPAQAGTDLNNPDLVSDATVSEKTLFW 234
Db 178 QSSQWPCAPGKFFGRGPIQLSHNYGPAQAGTDLNNPDLVSDATVSEKTLFW 237
QY 235 MTPQSPKPSHVDVTGRWSPSGADQAGRPVGVYNTNIINGLEGCGRQDGRVADRIGF 294
Db 238 MTPQSPKPSCHAVNTGQWTPNGNDQAGRPVGVYNTNIINGLEGCGRQDGRVADRIGF 297

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QY 295 YKRYCDLLGYSYGNLDCYNORPF 318
      |||||:|||||:|||||:|||||
Db 298 YKRYCDMLGVSIGANLDCYNORPF 321
      |||||:|||||:|||||:|||||

RESULT 5
S40414
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S40414
R:Nishizawa, Y.
submitted to the EMBL Data Library, November 1990
A:Reference number: S40414
A:Accession: S40414
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-340 <NIS>
A:Cross-references: EMBL:X56787; NID:g407471; PID:CAA40107.1; PID:g407472
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
F:92-330/Domain: plant chitinase homology <PCH>

Query Match 74.6%; Score 1317.5; DB 2; Length 340;
Best Local Similarity 72.4%; Pred. No. 1e-90;
Matches 228; Conservative 36; Mismatches 50; Indels 1; Gaps 1;

QY 4 VVAVMLAAAFSAHAECGSOAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQNGCSG 63
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 16 LVAVLAAALATAARAECCGAGARCPNCLCCSRWGCCTSDFCGDCGQSCSGC- 74

QY 64 GTPTVPPTPSGGVSSIIISQSLFDQMLLRNDACLAGFNYGAFVAAANSFSGFATT 123
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 GTPTPTPSDGSIVPRDLFERLLLRNDGACPARGFYTFEAFVAAAFPAFGGT 134

QY 124 GSTDVKKREVAFLAOTSHETGGWPTAPDGPYSWCYCFNOERGATSDYCTPSSOWPCAP 183
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 GNTETKREVAFLGOTSHETGGWPTADGPFWSWYCFKQEQNPSPDYCQSPENPCAP 194

QY 184 GKRYGRGPIQISHNINYPGAGQAIGTDLNPNPDVLSATVSKTALWFWMTPOQPKPSS 243
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 GRKYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDVATVSKTALWFWMTPOQNKPPS 254

QY 244 SHDVTGRWSPSGADAAAGRPVGYVTNIINGLCEGRCQDGRVADRIGFYKRYCDLLG 303
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 255 SHDVTGRWAPSPADAAAGRAPGYVTNIVNGLECGHGPDDRVANRIGFYQRYCGAFG 314

QY 304 VSYGDNLDYCNORPF 318
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 315 IGUGNLDYCNORPF 329

RESULT 6
S39979
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S39979
R:Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A:Title: Sequence variation, differential expression and chromosomal location of rice ch
A:Reference number: S39979; MUID:94049667
A:Accession: S39979
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <NIS>
A:Cross-references: EMBL:X56787
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:33-74/Domain: hevein chitin-binding domain homology <HCB>
```

F:91-329/Domain: plant chitinase homology <PCH>

```
Query Match 74.4%; Score 1313; DB 2; Length 339;
Best Local Similarity 72.9%; Pred. No. 2.2e-90;
Matches 229; Conservative 36; Mismatches 47; Indels 2; Gaps 2;

QY 5 VVAVMLAAAFSAHAECGSOAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQNGCSG 64
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 17 VALAVLAAALATAARAECCGAGARCPNCLCCSRWGCCTSDFCGDCGQSCSGGP 76

QY 65 GTPVPPTPSGGVSSIIISQSLFDQMLLRNDACLAGFNYGAFVAAANSFSGFATTG 124
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 TTPTP-PSPS-DGVGSIIVPRDLFERLLLRNDGACPARGFYTFEAFVAAAFPAFGGTG 134

QY 125 STDVKKREVAFLAOTSHETGGWPTAPDGPYSWCYCFNOERGATSDYCTPSSOWPCAPG 184
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 NFETKREVAFLGOTSHETGGWPTADGPFWSWYCFKQEQNPSPDYCQSPENPCAPG 194

QY 185 KRYFGRGPIQISHNINYPGAGQAIGTDLNPNPDVLSATVSKTALWFWMTPOQPKPSS 244
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 RXYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDVATVSKTALWFWMTPOQNKPPS 254

QY 245 HDVITGRWSPSGADAAAGRPVGYVTNIINGLCEGRCQDGRVADRIGFYKRYCDLLGV 304
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 255 HDVITGRWAPSPADAAAGRAPGYVTNIVNGLECGHGPDDRVANRIGFYQRYCGAFGI 314

QY 305 SYGDNLDYCNORPF 318
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 315 GTGGNLDYCNORPF 328

RESULT 7
S15997
Chitinase (EC 3.2.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C:Accession: S15997
R:Zhu, Q.; Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A:Title: Isolation and characterization of a rice gene encoding a basic chitinase.
A:Reference number: S15997; MUID:91238706
A:Accession: S15997
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <MOL>
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:22-63/Domain: hevein chitin-binding domain homology <HCB>
F:81-320/Domain: plant chitinase homology <PCH>
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Query Match 73.7%; Score 1301.5; DB 2; Length 336;
Best Local Similarity 72.3%; Pred. No. 1.5e-89;
Matches 237; Conservative 27; Mismatches 47; Indels 17; Gaps 4;

QY 1 MRGVVVVYVAMLAALAF-AVSAHAECGSOAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQ 59
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MRALAVVAVYVAPFLAAAVHAECGSOAGGAVCPNCLCCSQFGWCGSTSDYCGAGCQSQ 60

QY 60 N-----GCSGGTVPVPTPSGGVSSIIISQSLFDQMLLRNDACLAGFNYGAFVA 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SRLRRRPDASGG-----GGSGVASIVSRSLFDMLLRNDACPAFNFTYIDAFVA 112

QY 113 AANSFSQFATTGSDVKKREVAFLAOTSHETGGWPTADGPFWSWYCFNOER-GAITS 171
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 113 AASAFPFGAAGADATNKRVAFLAOTSHETGGWATADGPPYTWGYCFKEENGAGPD 172

QY 172 YCTPSSOWPCAPGKKYGRGPIQISHNINYPGAGQAIGTDLNPNPDVLSATVSKTAL 231
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 173 YCQQAQWPCAAGKKYGRGPIQLSFNFNYGPAGRAIGADLIGDPLVSDATVSEFTAF 232

QY 232 WFWMTPOSPKPSHSDVITGRWSPSGADAAAGRPVGYVTNIINGLCEGRCQDGRVADR 291
```

Db 233 WFWMTQSPKPCSNATATQWTFPSADQQRAGRVPGVITNIINGGLECGHGEDDRIADR 292
QY 292 IGFYKRYCDLLGVSYGNDLDCYNORPFA 319
Db 293 IGFYKRYCDILGVSYGANLDCYSORPSA 320

RESULT 8
T04484
A: Molecule type: DNA
A: Residues: 1-332 <LEA>
A: Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961
C: Species: Hordeum vulgare (barley)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C: Accession: T04484
R: Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A: Title: Identification of an enhancer/silencer sequence directing the aleurone-specific
A: Reference number: Z15373; MUID:95078949
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-332 <LEA>
A: Cross-references: EMBL:L34211; NID:g576566; PIDN:AAA56787.1; PID:g507961
C: Genetics:

A: Gene: Chi33
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; probable chitinase (EC 3.2.1.14) - barley
C: Keywords: glycosidase; hydrolase; polysaccharide degradation
F: 28-69/Domain: hevein chitin-binding domain homology <HCB>
F: 85-322/Domain: plant chitinase homology <PCH>

Query Match 73.2%; Score 1291.5; DB 2; Length 332;
Best Local Similarity 71.6%; Pred. No. 8.4e-89;
Matches 235; Conservative 33; Mismatches 43; Indels 17; Gaps 6;

QY 1 MRG-----VVVYMLAAAFVSAHAEOCGSQAGGATCPNCLCCSKFPGCGTSDYCGT 53
Db 1 MRGFSVVYVAIVAIYLSAALAMAYVRAQCGSQAGGATCPNCLCCSKRPGYCGSTDYCGA 60

QY 54 GCQSQCGCGTGPVPTPGSGGVSSISQSLFDQMLLHRN---DAACIAKAGFYNGAF 110

Db 61 GCQSQCGSC-GPTP-PGESP-GGGVSSISRDLEQFLHHRDQDAA---GYTYDAF 113

QY 111 VAAANSFGFATGSTDVKKREVAFAIAQTSHETTGWPTAPDGPYSWGYCFNBERGATS 170

Db 114 LARAATPAFGTGTETRKQEVAAFFQGTSHETTGWATAPDGPYSWGYCYRRELGSPP 173

QY 171 DYCTPSSOWPCAPGKKYFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSEKTA 230

Db 174 DYCPSSOWPCVQDQRYTGRGPIMLSWNYNGPAGRAIGVLDLNNPDVADATVSEKTA 233

QY 231 LWFWMTPQSPKPSHDVITGRWSPSGADQAGRVPGYVITNIINGGLECGRGQDGRVAD 290

Db 234 LWFWMTPQANKPSSHAVITGQWTPAATAAGRVPGYVITNIINGGLECGRGADSRVAD 293

QY 291 RIGFYKRYCDLLGVSYGNDLDCYNORPF 318

Db 294 RIGFYQRYCNILGVGYGGNLDYCNORPF 321

RESULT 9
S14948
A: Molecule type: DNA
A: Residues: 1-329 <SHI>
A: Cross-references: EMBL:X16938; NID:g19860; PIDN:CAA34812.1; PID:g19861
A: Experimental source: cv. Havana 425
R: Neale, A.D.; Wahleithner, J.A.; Lund, M.; Bonnett, H.T.; Kelly, A.; Meeks-Wagner, D.
Plant Cell 2, 673-684, 1990
A: Title: Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in tobacco
A: Reference number: JQ0993; MUID:92404740
A: Accession: JQ0993
A: Molecule type: mRNA
A: Residues: 1-72, 'H', 74, 'TRC', 79-262, 'S', 264-329 <NEA>
A: Cross-references: GB:S44869; NID:g256132; PIDN:AAB23374.1; PID:g256133
A: Experimental source: thin cell layer, cv. samsun nn
C: Comment: This protein is expressed mainly in roots.
C: Genetics:
A: Introns: 148/1; 199/2
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
N: Alternate names: class I endochitinase
C: Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C: Accession: S14948
R: Huang, J.K.; Wen, L.; Swegle, M.; Tran, H.C.; Thin, T.H.; Naylor, H.M.; Muthukrishnan,
Plant Mol. Biol. 16, 479-480, 1991
A: Title: Nucleotide sequence of a rice genomic clone that encodes a class I endochitinase
A: Reference number: S14948; MUID:91370895
A: Accession: S14948
A: Status: preliminary

A: Molecule type: DNA
A: Residues: 1-318 <HUA>
A: Cross-references: EMBL:X54367; NID:g20195; PIDN:CAA38249.1; PID:g20196
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C: Keywords: glycosidase; hydrolase; polysaccharide degradation
F: 19-60/Domain: hevein chitin-binding domain homology <HCB>
F: 79-316/Domain: plant chitinase homology <PCH>

Query Match 73.1%; Score 1289.5; DB 2; Length 318;

Best Local Similarity 73.4%; Pred. No. 1.1e-88;
Matches 234; Conservative 24; Mismatches 56; Indels 5; Gaps 4;

QY 1 MRGWWVYMLAAAFVSAHAEOCGSQAGGATCPNCLCCSKFPGCGTSDYCGTSGQSQCN 60

Db 1 MRALAAVAMAVAV--RCEQCGSQAGGALCPNCLCCSQYGCWGSTSDYCGAGCQSCS 58

QY 61 GCSGGTGPVPTPGSGGVSSISQSLFDQMLLHRNDAACIAKAGFYNGAFVAAANSFSGF 120

Db 59 GCGGGTPTPPSGGGGVASIIISPLFDQMLLHRNDQACRAKGFYTYDAVAAANAYPDF 118

QY 121 ATTGSTDVKKREVAFAIAQTSHETTGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSOW 179

Db 119 ATTRDADTCREVAFAIAQTSHETTGWPTAPDGPYSWGYCFKEENNGNAPTCEPKPEW 178

QY 180 PCAPKKYFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSEFKTALNFWMTPOS 239

Db 179 PCAAKKYFGRGPIQITINYNG-RGAGIGSDLLNPDVADATVSEFKTAFWMTPOS 236

QY 240 PKSSHVDITGRWSPSGADQAGRVPGYVITNIINGGLECGRGQDGRVADRIGFYKRYC 299

Db 237 PKPSCHAVITGQWTPSADQAGRVPGYGETNIINGVCEGEGHGDVADRIGFYKRYC 296

QY 300 DLLGVSYGNDLDCYNORPF 318

Db 297 DMLGVSYGNDLDCYNORPF 315

RESULT 10

S08627
A: Molecule type: DNA
A: Residues: 1-329 <SHI>
A: Cross-references: EMBL:X16938; NID:g19860; PIDN:CAA34812.1; PID:g19861
A: Experimental source: cv. Havana 425
R: Neale, A.D.; Wahleithner, J.A.; Lund, M.; Bonnett, H.T.; Kelly, A.; Meeks-Wagner, D.
Plant Cell 2, 673-684, 1990
A: Title: Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in tobacco
A: Reference number: S08627; MUID:91345623
A: Accession: S08627
A: Molecule type: DNA
A: Residues: 1-329 <SHI>
A: Cross-references: EMBL:X16938; NID:g19860; PIDN:CAA34812.1; PID:g19861
A: Experimental source: cv. Havana 425
R: Neale, A.D.; Wahleithner, J.A.; Lund, M.; Bonnett, H.T.; Kelly, A.; Meeks-Wagner, D.
Plant Cell 2, 673-684, 1990
A: Title: Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in tobacco
A: Reference number: JQ0993; MUID:92404740
A: Accession: JQ0993
A: Molecule type: mRNA
A: Residues: 1-72, 'H', 74, 'TRC', 79-262, 'S', 264-329 <NEA>
A: Cross-references: GB:S44869; NID:g256132; PIDN:AAB23374.1; PID:g256133
A: Experimental source: thin cell layer, cv. samsun nn
C: Comment: This protein is expressed mainly in roots.
C: Genetics:
A: Introns: 148/1; 199/2
C: Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C: Keywords: glycosidase; hydrolase; polysaccharide degradation
F: 1-23/Domain: signal sequence #status predicted <SIG>
F: 24-329/product: chitinase #status predicted <MAT>
F: 24-66/Domain: hevein chitin-binding domain homology <HCB>
F: 83-321/Domain: plant chitinase homology <PCH>

A:Residues: 1-324 <MEI>
A:Cross-references: EMBL:X64519; NID:g19846; PIDN:CAA45822.1; PID:g19847
A:Experimental source: cv. Havana 425
R:Shinshi, H.; Mohnen, D.; Havens Jr., F.
Proc. Natl. Acad. Sci. U.S.A. 84, 89-93, 1987
A:Title: Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and
A:Reference number: A29074
A:Accession: A29074
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 15-324 <SHI>
R:Fukuda, Y.; Ohme, M.; Shinshi, H.
Plant Mol. Biol. 16, 1-10, 1991
A:Title: Gene structure and expression of a tobacco endochitinase gene in suspension-cul
A:Reference number: S13322; MUID:91363829
A:Accession: S13322
A:Molecule type: DNA
A:Residues: 1-324 <FOK>
A:Cross-references: EMBL:X51599; NID:g19844; PIDN:CAA35945.1; PID:g19845
A:Experimental source: cv. BY4
C:Genetics:
A:Introns: 143/1; 194/2
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-324/Product: chitinase B #status predicted <MAT>
F:24-66/Domain: hevein chitin-binding domain homology <HCB>
F:76-316/Domain: plant chitinase homology <PCH>

Query Match 71.4%; Score 1261; DB 2; Length 324;
Best Local Similarity 72.1%; Pred. No. 1.5e-86;
Matches 225; Conservative 29; Mismatches 50; Indels 8; Gaps 3;

QY 8 AMLAARAVSAHAEQCSQAGATCPNCLCSKFGCGTTSDYCGTG-CQSQCNGCSGGT 66
Db 11 SLFLSLLLSASACQCSQAGARACAGLCCSKFGCGTNDYCGPGNCQCCPG--GPT 68
QY 67 PVVPTPSGGVSSIIQSOLFQMLLRNDAAKLAGFYNYGAFVAANSPSGFATTGST 126
Db 69 P-----PGGDLGSISSSMFQMLKLRNDNACQCKGKGFYSYNAFINAARSPFGTSDT 123
QY 127 DVKKREVAFAQTSHETTGWPTAPDGPYSGWYCFNQRGATSDYCTPSSQWPCAPGK 186
Db 124 TARKREIAAFAQTSHETTGWPTAPDGPYAWGYCFLREQSGPDYCTPSSQWPCAPGK 183
QY 187 YFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSHD 246
Db 184 YFGRGPIQISHNYNGPAGRAIGVDLLNPDVADTVPISFKSAFWMTPOSPPSCHD 243
QY 247 VITGRWSPGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGVSY 306
Db 244 VITGRWSPSSADRAANRUPGFGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGVSP 303
QY 307 GDNLDYCNORPF 318
Db 304 GDNLDYCNORSF 315

RESULT 14
S65019
chitinase (EC 3.2.1.14) precursor (clone Chtb1) - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C:Accession: S65019
R:Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
A:Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-beta
A:Reference number: S43317; MUID:94154255
A:Accession: S65019
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-318 <BEE>

A:Cross-references: EMBL:U02605; NID:g467819; PIDN:AAA18332.1; PID:g467820
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase
F:19-61/Domain: hevein chitin-binding domain homology <HCB>
F:71-310/Domain: plant chitinase homology <PCH>

Query Match 71.1%; Score 1255.5; DB 2; Length 318;
Best Local Similarity 72.6%; Pred. No. 3.8e-86;
Matches 228; Conservative 26; Mismatches 45; Indels 15; Gaps 5;

QY 9 MLAARAVSAHAEQCSQAGATCPNCLCSKFGCGTTSDYCGTG-CQSQCNGCSGGT 67
Db 7 LFLSLLLSASACQCSQAGALCASGLCCSKFGCGTNDYCGPGNCQCCPG----- 60
QY 68 VPVPTPSG--GGVSSIIQSOLFQMLLRNDAAKLAG--FYNYGAFVAANSPSGFATTG 124
Db 61 --GGPSPGDLGGV--ISNSMFQMLNHRNDNACQCKGKGFYSYNAFINAAGSPFGTGT 115
QY 125 STDVKKREVAFAQTSHETTGWPTAPDGPYSGWYCFNQRGATSDYCTPSSQWPCAPG 184
Db 116 DITARKREIAAFAQTSHETTGWPTAPDGPYAWGYCFLREQSGPDYCTPSSQWPCAPG 175
QY 185 KKYFGRGPIQISHNYNGPAGQATGTDLLNPDVADATVSKFTALFWMTPOSPPSS 244
Db 176 KKYFGRGPIQISHNYNGPAGRAIGVDLLNPDVADTVPISFKSAFWMTPOSPPSC 235
QY 245 HDVITGRWSPGADQAGRPVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLGV 304
Db 236 HDVITGRWSPGVDQANRVPFGVITNIINGGLECGHSGDSRVQDRIGFYKRYCGILGV 295
QY 305 SYGNDLCYNORPF 318
Db 296 SPGNDLCGNORSF 309

RESULT 15
S43317
chitinase (EC 3.2.1.14) class I precursor (clone ChtB3) - potato (fragment)
N:Alternate names: basic chitinase precursor
C:Species: Solanum tuberosum (potato)
C:Date: 20-Oct-1994 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C:Accession: S43317; S06161
R:Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
A:Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-b
A:Reference number: S43317; MUID:94154255
A:Accession: S43317
A:Molecule type: mRNA
A:Residues: 1-318 <BEE>
A:Cross-references: EMBL:U02607; NID:g467823; PIDN:AAA17409.1; PID:g467824
R:Laflamme, D.; Roxby, R.
Plant Mol. Biol. 13, 249-250, 1989
A:Title: Isolation and nucleotide sequence of cDNA clones encoding potato chitinase g
A:Reference number: S06161; MUID:92003671
A:Accession: S06161
A:Molecule type: mRNA
A:Residues: 3-17, 'GSNVVHRED', 28-234, 'X', 236-318 <LAF>
A:Cross-references: EMBL:X14133; NID:g21464; PIDN:CAA32351.1; PID:g21465
A:Note: the authors translated the codon CAG for residues 54 and 303 as Gly, YGC for
Y
C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:19-311/Product: chitinase #status predicted <MAT>
F:19-61/Domain: hevein chitin-binding domain homology <HCB>
F:71-310/Domain: plant chitinase homology <PCH>
F:312-318/Domain: carboxyl-terminal propeptide #status predicted <PRO>

Query Match 70.8%; Score 1250.5; DB 2; Length 318;
Best Local Similarity 71.6%; Pred. No. 8.9e-86;
Matches 227; Conservative 29; Mismatches 46; Indels 15; Gaps 5;

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QY 6 VVAMLAFAVSAHAEOCSQAGATCPNCLCCSKFCGTTSDYCGTG-CQSQCNCSG 64
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
4 IFSLLFSLLLINASAEQCSQAGGALCAPLCCSKFGWCNTINDYCGPNCQSQCPG-- 60
QY 65 GTPVPVPTPSG--GGVSSIIISQSLFQMLLHRNDAACLAKE-GEYNYGAFVAAANSFSGFA 121
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
61 -----GCPSPGDLGGV--ISNSMFDQMLNHRNDNACQGNFYNAFISAAGSFFPGFG 112
QY 122 TTGSTDVKKREVAFLAOTSHETITGGWFTAPDGPYSWGYPNQERGATSDYCTPSSQWPC 181
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
113 TTGDITARKREIAFLAQTSHETITGGWPSAPDGPYAWGYCFLREQSGPDYCTPSSQWPC 172
QY 182 APGRKYFCRGPQIUSHNYNGYPAGQAIGTDLNNPDLVASDATYSFKTALWFWMTPOS PK 241
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
173 APGRKYFCRGPQIUSHNYNGYPAGQAIGTDLNNPDLVASDATYSFKTALWFWMTPOS PK 232
QY 242 PSSHDVITGRWSPSGAQAGRVFGYGYITNIINGGLECGRGQDGRVADRIGFYKRYCDL 301
Db :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
233 PSCHDVITGRWQPSGADQAANRVPGFVITNIINGGLECGHGSDSRVQDRIGFYRRYCGI 292
QY 302 LGVSYGDNLDYINORPF 318
Db :::: :::: :::: :::: :::: :::: :::: :::: ::::
293 LGVSPGDNLDYINORSE 309
```

Search completed: May 3, 2002, 18:32:13
Job time: 7476 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:48:32 ; Search time 78.59 seconds
(without alignments)
148.824 Million cell updates/sec

Title: US-09-534-229c-3

Perfect score: 1765

Sequence: 1 MRGVVVVMAAAFAVSAHA.....DLIGVSYGNLDCYNORPFA 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1407.5	79.7	318	1 CH11_HORVU	P11955 hordeum vul
2	1301.5	73.7	336	1 CH12_ORYSA	P25765 oryza sativ
3	1289.5	73.1	318	1 CH11_ORYSA	P24626 oryza sativ
4	1281.5	72.6	329	1 CH11_TOBAC	P08252 nicotiana t
5	1261.5	71.4	324	1 CH12_TOBAC	P24091 nicotiana t
6	1255.5	71.1	318	1 CH11_SOLTU	P52403 solanum tub
7	1250.5	70.8	318	1 CH13_SOLTU	P52405 solanum tub
8	1248.5	70.7	322	1 CH1C_LYCES	O05538 lycopersico
9	1240.5	70.3	316	1 CH12_SOLTU	P52404 solanum tub
10	1215	68.8	320	1 CH1X_PEA	P36907 pisum sativ
11	1208	68.4	324	1 CH12_PEA	P21226 pisum sativ
12	1208	68.4	328	1 CH1T_SOLTU	P05315 solanum tub
13	1206	68.3	334	1 CH13_TOBAC	P29059 nicotiana t
14	1193.5	67.6	302	1 CH14_SOLTU	P52406 solanum tub
15	1192.5	67.6	322	1 CH14_BRANA	O09023 brassica na
16	1190.5	67.5	322	1 CH1T_ARATH	P19171 arabidopsis
17	1187.5	67.3	314	1 CH1B_VITVI	P51613 vitis vinif
18	1183	67.0	328	1 CH1T_PHAVU	O05538 lycopersico
19	1178.5	66.8	324	1 CH11_GOSHI	P36361 phaseolus v
20	1168.5	66.2	327	1 CH15_PHAVU	O05538 lycopersico
21	1154.5	65.4	302	1 CH12_GOSHI	P39785 gossypium h
22	1151.5	65.2	321	1 CH11_THECC	O41596 theobroma c
23	1125	63.7	266	1 CH12_HORVU	P23951 hordeum vul
24	1022.5	57.9	340	1 CH16_POPTR	P16579 populus tri
25	1004	56.9	246	1 CH1D_LYCES	O05537 lycopersico
26	874.5	49.5	303	1 CH1B_POPTR	P29031 populus tri
27	805.5	45.6	254	1 CH1T_PETHY	P29021 petunia hyb
28	803.5	45.5	316	1 CH18_POPTR	P16061 populus tri
29	791.5	44.8	247	1 CH1B_LYCES	O05540 lycopersico
30	785.5	44.5	253	1 CH1C_TOBAC	P17514 nicotiana t
31	763.5	43.3	253	1 CH1P_TOBAC	P11213 nicotiana t
32	722.5	40.9	372	1 AG1_URTDI	P11218 urtica dioi
33	712.5	40.4	253	1 CH1A_LYCCI	Q40114 lycopersico

RESULT 1	CH11_HORVU	253	1	CH1A_LYCES	Q05539 lycopersico
ID	CH11_HORVU	STANDARD;	PRT;	318 AA.	P42820 beta vulgar
AC	P11955;				P29023 zea mays (m
DT	01-OCT-1989 (Rel. 12, Created)				Q06209 brassica na
DT	01-NOV-1997 (Rel. 35, Last sequence update)				P29022 zea mays (m
DT	01-NOV-1997 (Rel. 35, Last annotation update)				P27054 phaseolus v
DE	26 KDA ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14).				P80052 dioscorea j
OS	Hordeum vulgare (Barley).				P29032 populus tri
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				P15326 colx lachry
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				Q06015 arachis hyp
OC	Triticeae; Hordeum.				P15312 hordeum vul
OX	NCBI_taxID=4513;				Q06012 arachis hyp
[1]					
RP	SEQUENCE FROM N.A.				
RC	STRAIN-CV. NK 1558; TISSUE=Leaf;				
RA	Ignatius S.M.J.; Huang J.; Muthukrishnan S.;				
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.				
[2]					
RP	SEQUENCE OF 141-318 FROM N.A.				
RC	STRAIN-CV. HIMALAYA;				
RA	Swiegie M.; Huang J.-K.; Lee G.; Muthukrishnan S.;				
RT	"Identification of an endochitinase cDNA clone from barley aleurone cells.";				
RL	Plant Mol. Biol. 12:403-412(1989).				
CC	-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN				
CC	-!- CONTAINING FUNGAL PATHOGENS.				
CC	-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF				
CC	-!- N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.				
CC	-!- INDUCTION: BY ETHYLENE.				
CC	-!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO				
CC	-!- CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL				
CC	CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL				
CC	HYDROLASES).				
CC	-----				
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CC	-----				
CC	EMBL; U02287; AAA18586.1; -				
DR	EMBL; X15349; CAA33407.1; -				
DR	PIR; S04131; S04131.				
DR	HSSP; P23951; 2BAA.				
DR	InterPro; IPR001002; Chitin_bind.				
DR	InterPro; IPR000726; Glyco_hydro_19.				
DR	Pfam; PF00187; chitin_binding_1.				
DR	Pfam; PF00182; Glyco_hydro_19; 1.				
DR	PRINTS; PR00451; CHITINBINDING.				
DR	ProDom; PD000574; Glyco_hydro_19; 1.				
DR	ProDom; PD000609; Chitin_bind; 1.				
DR	SMART; SM00270; ChitBD1.				
DR	PROSITE; PS00773; CHITINASE_19_1; 1.				


```

RL Plant Mol. Biol. 16:479-480(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC -----
CC EMBL; X54367; CAA38249.1; -.
CC DR PIR; S14948; S14948.
CC DR HSP; P02877; LHEV.
CC DR InterPro; IPR001002; Chitin_bind.
CC DR InterPro; IPR000726; Glyco_hydro_19.
CC DR Pfam; PF00187; chitin_binding; 1.
CC DR PRINTS; PR00451; CHITINBINDNG.
CC DR ProDom; PD000574; Glyco_hydro_19; 1.
CC DR ProDom; PD000609; Chitin_bind; 1.
CC DR SMART; SM00270; ChitBD1; 1.
CC DR PROSITE; PS00026; CHITIN_BINDING; 1.
CC DR PROSITE; PS00773; CHITINASE_19_1; 1.
CC DR PROSITE; PS00774; CHITINASE_19_2; 1.
CC DR Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Multigene family.
CC FT SIGNAL 1 18 POTENTIAL.
CC FT CHAIN 19 318 BASIC ENDOCHITINASE 1.
CC FT DOMAIN 19 61 CHITIN-BINDING (BY SIMILARITY).
CC FT DISULFID 21 36 BY SIMILARITY.
CC FT DISULFID 30 42 BY SIMILARITY.
CC FT DISULFID 35 49 BY SIMILARITY.
CC FT DISULFID 53 57 BY SIMILARITY.
CC SEQUENCE 318 AA; 33695 MW; 8FD37913450CC7EB CRC64;

Query Match 73.1%; Score 1289.5; DB 1; Length 318;
Best Local Similarity 73.4%; Pred. NO. 5.7e-90;
Matches 234; Conservative 24; Mismatches 56; Indels 5; Gaps 4;

QY 1 MRGVVVAIAAFAVSAHAECQSGAGATCPNCLCSKFCGCTTSDYCGTGCSQCN 60
DB 1 MRATALAVVAMAVAV--RGEQCSQAGALCPNCLCSQYGCWGSTDYCGAGCSQCS 58
QY 61 GCSGCTPVPPPPSGGVSIIISLFQDMLLRNDAACLRKGFYNYGAFVAAANSFSGF 120
DB 59 GCGCGGPPPPSGGSGVASIIISLFQDMLLRNDAQACRAKGFYDYAFVAAANAYPDF 118
QY 121 ATGTSTDVKKREVAFLAQTSHETTGWPTADPGYSWGYCFNQE--RGATSDYCTPSSQW 179
DB 119 ATTRDADTKREVAFLAQTSHETTGWPTADPGYSWGYCFKEENGNAPTCEFKPEW 178
QY 180 PCAPGKKEVGRPIQISHNRYNYPGQAQATGTLNPNPDVASDATVSEKTLKFWMTPOS 239
DB 179 PCAARKKYYGRPIQITYNYNGY--RGAGTGSLLNPNPDVASDA--VSFKTAFWFWMTPOS 236
QY 240 KPSSHDVITGRWPSGADQAAGRVPGYVITNINIGGLECGRGQDGRVADRIGFYKRYC 299
DB 237 KPFSCHAVITGQWTPSADQAAGRVPGYGEITNININGVECGHGADDKVADRIGFYKRYC 296
QY 300 DLGVSYGDNLDYCNQRP 318
DB 297 DMLGVSYGDNLDYCNQRP 315

```

```

RESULT 4
CHIL_TOBAC
ID CHIL_TOBAC STANDARD; PERT; 329 AA.
AC P08252;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
GN CHN48.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAVANA 425; TISSUE=Leaf;
RX MEDLINE=51346623; PubMed=1966383;
RA Shinshi H., Neuhaus J.-M., Fyals J., Meins F. Jr.;
RT "Structure of a tobacco endochitinase gene: evidence that different
RT chitinase genes can arise by transposition of sequences encoding a
RT cysteine-rich domain.";
RL Plant Mol. Biol. 14:357-368(1990).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=32052270; PubMed=1946457;
RA Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
RT targeting of chitinases to the plant vacuole.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
RN [3]
RP HYDROXYLATION.
RX MEDLINE=92358209; PubMed=1496378;
RA Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
RT containing proteins.";
RL Science 257:655-657(1992).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- INDUCTION: BY ETHYLENE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
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CC -----
CC EMBL; X16938; CAA34812.1; -.
CC DR EMBL; X16939; CAA34813.1; -.
CC DR PIR; S08627; S08627.
CC DR HSP; P23951; 2BAA.
CC DR InterPro; IPR001002; Chitin_bind.
CC DR InterPro; IPR000726; Glyco_hydro_19.
CC DR Pfam; PF00187; chitin_binding; 1.
CC DR Pfam; PF00182; Glyco_hydro_19; 1.
CC DR PRINTS; PR00451; CHITINBINDNG.
CC DR ProDom; PD000574; Glyco_hydro_19; 1.
CC DR ProDom; PD000609; Chitin_bind; 1.
CC DR SMART; SM00270; ChitBD1; 1.
CC DR PROSITE; PS00026; CHITIN_BINDING; 1.
CC DR PROSITE; PS00773; CHITINASE_19_1; 1.
CC DR PROSITE; PS00774; CHITINASE_19_2; 1.
CC DR Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Hydroxylation; Multigene family.

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FT SIGNAL 1 23
FT CHAIN 24 322
FT PROPEP 323 329
FT DOMAIN 24 65
FT DISULFID 26 41
FT DISULFID 35 47
FT DISULFID 40 54
FT DISULFID 59 63
FT MOD_RES 67 67
FT MOD_RES 69 69
FT MOD_RES 71 71
FT MOD_RES 72 72
FT MOD_RES 74 74
FT MOD_RES 75 75
FT SEQUENCE 329 AA; 35156 MW; 3EC99D96E6C0114C CRC64;

Query Match 72.6%; Score 1281.5; DB 1; Length 329;
Best Local Similarity 73.2%; Pred. No. 2.4e-89;
Matches 229; Conservative 29; Mismatches 50; Indels 5; Gaps 4;

QY 8 AMLAAAFNYSAAHAEQGSQAGGATPCNLCCKSKFGCTSDYCGTG-CQSQCNCGSGGT 66
Db 11 SLIFSULLLSASAEQGSQAGGARGCPSCGLCCSKFGCGTNDYCGPNCOSQCPG--GPT 68
QY 67 PVPPTPSGGG-VSSISQSFLDQMLLHRNDAAACLAGFYNYGAFVAAANSFSGFATGGS 125
Db 69 PTP-PTPPGGDLGSISSSMFDMKLKRNACQKGFYSYNAFINAARSFPFGTSGD 127
QY 126 TDVKKREVAFLAQTSHETGGTAPDPGYSWGYCNFNGRGATSDYCPSSWPCAPGK 185
Db 128 TARKKEIAAFAQTSHETGGWATAPDGPYAWGYCWLREQSPGDCYCTPSGOWPCAPGR 187
QY 186 KYFGRGPIQTSNHNKYPGAGQATGTLNPNPLVADATVSEKTLFWMTWTPSPKPSHH 245
Db 188 KYFGRGPIQTSNHNKYPGAGQATGTLNPNPLVADATVSEKTLFWMTWTPSPKPSCH 247
QY 246 DVTIGRWSPGADQAGRPVGYVNIINGLECGRGQGRVADRIGFYKRYCDLLGVS 305
Db 248 DVTIGRWSPGADQAGRNRLPFGVITNIINGLECGRGTSRVQDRIGFYKRYCSILGVS 307
QY 306 YGDNLCYNORPF 318
Db 308 PGDNLDGNGRNF 320

RESULT 5
CH12_TOBAC STANDARD; PRT; 324 AA.
AC P24091;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
GN CHN50.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BRIGHT YELLOW 4; TISSUE=Leaf;
RX MEDLINE=91363829; PubMed=188889;
RA Fukuda Y., Ohme M., Shinshi H.;
RT "Gene structure and expression of a tobacco endochitinase gene in
RT suspension-cultured tobacco cells.";
RL Plant Mol. Biol. 16:1-10(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAVANA 425; TISSUE=Leaf;
RX MEDLINE=92269767; PubMed=1588915;
RA van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;

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RT "The structure and regulation of homeologous tobacco endochitinase
RT genes of Nicotiana sylvestris and N. tomentosiformis origin.";
RL Mol. Gen. Genet. 232:460-469(1992).
[3]
RN SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
RC STRAIN=CV. HAVANA;
RA Shinshi H., Mohnen D., Meins F. Jr.;
RT "Regulation of a plant pathogenesis-related enzyme: inhibition of
RT chitinase and chitinase mRNA accumulation in cultured tobacco tissues
RT by auxin and cytokinin.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:89-93(1987).
[4]
RN SUBCELLULAR LOCATION.
RP MEDLINE=92052270; PubMed=1946457;
RX Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
RT "A short C-terminal sequence is necessary and sufficient for the
RT targeting of chitinases to the plant vacuole.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
[5]
RN HYDROXYLATION.
RP MEDLINE=92358209; PubMed=1496378;
RX Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr.;
RT "Vacuolar chitinases of tobacco: a new class of hydroxyproline-
RT containing proteins.";
RL Science 257:655-657(1992).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF CHITIN.
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
CC -!- INDUCTION: BY ETHYLENE.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDES A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
-----
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CC or send an email to license@isb-sib.ch).
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EMBL; X51599; CAA35945.1; -;
DR EMBL; X64519; CAA45822.1; -;
DR EMBL; M15173; AAA34070.1; -;
DR PIR; A29074; A29074.
DR PIR; S13322; S13322.
DR PIR; S20981; S20981.
DR HSSP; P23951; ZBAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR Hydrolase; glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Hydroxylation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 317 ENDOCHITINASE B.
FT PROPEP 318 324 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION.

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FT MOD_RES 69 69 HYDROXYLATION.
SQ SEQUENCE 324 AA; 34721 MW; FA65DC2113B33EB6 CRC64;

Query Match 71.4%; Score 1263; DB 1; Length 324;
Best Local Similarity 72.1%; Pred. No. 8e-88;
Matches 225; Conservative 29; Mismatches 50; Indels 8; Gaps 3;

QY 8 AMLAAFAVSAHAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 66
Db 11 SLLSLLLSASAEQCGAGARCAAGLCCSKFGWCNTNDYCGNCGSQCPG--GPT 68
QY 67 PVPVPTSGGGVSSIIQSLEFDQMLLNHRNDAAKAGFYNYGAFVAANSPSGPATTGST 126
Db 69 P-----PGGDLGSIISSMFQMLKRNDAACQCKGFSYNAFINAAARSPFGTSGDT 123
QY 127 DVKKREVAFLAQTSHETGGWPTAPDGPYAWGYCWLEQGGSPGDCYTPSSQWPCAPGKK 186
Db 124 TARKREIAAFAQTSHETGGWATAPDGPYAWGYCWLEQGGSPGDCYTPSSQWPCAPGKK 183
QY 167 YFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSKTALWFMTQSPKPSHD 246
Db 164 YFGRGPIQISHNYNGPAGRAIGVDLLNNDLVATDPVISKSAFWMTQSPKPSCHD 243
QY 247 VITGRWSPGDAQAGRPVGYGVITNIINGLECGRGDGRVADRIGRYKRYCDLLGVSY 306
Db 244 VITGRWSPSADRAANRLPGFVITNIINGLECGRGDGRVADRIGRYKRYCISILGVSP 303
QY 307 GDNLDYCNORPF 318
Db 304 GDNLDYCNORSF 315

RESULT 6
CH13_SOLITU STANDARD; PRT; 318 AA.
ID CH13_SOLITU
AC P52403;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CH13.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=941154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
OLD ROOT SEGMENTS, AND CARPELS.
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
CC
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or send an email to license@isb-sib.ch).
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EMBL; U02605; RAA18332.1; -
HSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding_1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SMO0270; ChEBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT SIGNAL 1
FT NON_TER 1
FT CHAIN 18
FT CHAIN 19 311
FT PROPEP 312 318
FT
FT
FT DOMAIN 19 60
FT DISULFD 21 36
FT DISULFD 30 42
FT DISULFD 35 49
FT DISULFD 54 58
FT SEQUENCE 318 AA; 33813 MW; A0B49DA528706AAA CRC64;

Query Match 71.1%; Score 1255.5; DB 1; Length 318;
Best Local Similarity 72.6%; Pred. No. 2e-87;
Matches 228; Conservative 26; Mismatches 45; Indels 15; Gaps 5;

QY 9 MAAAFAYSAHAEQCGAGATPCNLCCKSKFGCTGTTSDYCGTG-CQSQCNCGSGGT 67
Db 7 LLFSVILLLSASAEQCGAGALCAGLCCSKFGWCGTNDYCGNCGSQCPG----- 60
QY 68 VFPVTPSG--GGVSSIIQSLEFDQMLLNHRNDAAKLAG-FYNYGAFVAANSPSGFATTG 124
Db 61 --GPGSGDLGV--ISNSMFDQMLNHRNDNAQCKGNFYNAFISAAGSPFGTGTG 115
QY 125 STDVKREVAFLAQTSHETGGWPTAPDGPYSWGYCENQERGATSDYCTPSQWPCAPG 184
Db 116 DITARKREIAAFAQTSHETGGWPTAPDGPYAWGYCWLEQGGSPGDCYTPSSQWPCAPG 175
QY 185 KYFGRGPIQISHNYNGPAGQAIGTDLNNDLVASDATVSKTALWFMTQSPKPS 244
Db 176 KYFGRGPIQISHNYNGPAGRAIGVDLLNNDLVATDSVISKSAFWMTQSPKPS 235
QY 245 HDVITGRWSPGDAQAGRPVGYGVITNIINGLECGRGDGRVADRIGRYKRYCDLLGV 304
Db 236 HDVITGRWSPGVDQAANRPVGYGVITNIINGLECGRGDGRVADRIGRYKRYCIGLV 295
QY 305 SYGDNLDYCNORPF 318
Db 296 SPGDNLDYCNORSF 309

RESULT 7
CH13_SOLITU STANDARD; PRT; 318 AA.
ID CH13_SOLITU
AC P52405;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CH13.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. DATURA; TISSUE=Leaf;
 RX MEDLINE=94154255; PubMed=8111037;
 RA Beerhues L., Kombrink E.;
 RT "Primary structure and expression of mRNAs encoding basic chitinase
 and 1,3-beta-glucanase in potato.";
 RL Plant Mol. Biol. 24:353-367(1994).
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
 CONTAINING FUNGAL PATHOGENS.
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
 N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
 CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
 SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
 SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
 OLD ROOT SEGMENTS, AND CARPELS.
 CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
 CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
 CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
 CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
 HYDROLASES).
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U02607; AAA17409.1; -.
 CC HSP; P23951; 2BAA.
 DR InterPro: IPR001002; Chitin_bind.
 DR InterPro: IPR000726; Glyco_hydro_19.
 DR Pfam; PF00187; chitin_binding; 1.
 DR Pfam; PF00182; Glyco_hydro_19; 1.
 DR ProDom; PD000574; Glyco_hydro_19; 1.
 DR ProDom; PD000609; Chitin_bind; 1.
 DR SMART; SM00270; CHCD1; 1.
 DR PROSITE; PS00026; CHITIN_BINDING; 1.
 DR PROSITE; PS00773; CHITINASE_19_1; 1.
 DR PROSITE; PS00774; CHITINASE_19_2; 1.
 KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
 KW Multigene family.
 FT NON_TER 1
 FT SIGNAL <1 18 POTENTIAL.
 FT CHAIN 19 311 REMOVED IN MATURE FORM, VACUOLAR
 FT PROPEP 312 318 TARGETING (POTENTIAL).
 FT FT DOMAIN 19 60 CHITIN-BINDING (BY SIMILARITY).
 FT FT DISULFID 21 36 BY SIMILARITY.
 FT FT DISULFID 30 42 BY SIMILARITY.
 FT FT DISULFID 35 49 BY SIMILARITY.
 FT FT DISULFID 54 58 BY SIMILARITY.
 SQ SEQUENCE 318 AA; 33798 MW; BF587A8515534E71 CRC64;

Query Match 70.8%; Score 1250.5; DB 1; Length 318;
 Best Local Similarity 71.6%; Pred. No. 4.8e-87;
 Matches 227; Conservative 29; Mismatches 46; Indels 15; Gaps 5;

Db 113 TTGDITARKREIAAFLAQTSHETTGGWPSAPDGPYANGYFLREQSGDGYCTPSSQWPC 172
 QY 182 APGKVFGRGPIQISHNNGYGPAGOAIGTDLNPNLDVADATVSKFTALWFMTQSPK 241
 Db 173 APGRKYFGRGPIQISHNNGYGPAGOAIGTDLNPNLDVADATVSKFTALWFMTQSPK 232
 QY 242 PSSHDVITGWSGADQAAAGRVPGYGVITNIIINGGLECGRGQDGRVADRIGRYKRYCDL 301
 Db 233 PSCHDVTGWSQFSGADQAAANRVPGYGVITNIIINGGLECGHSDSRVQDRIGRYRYCGI 292
 QY 302 LGVSYGDNLDYQWRF 318
 Db 293 LGVSPGDNLDGNGRSF 309
 RESULT 8
 CHIC_LYCES STANDARD; PRT; 322 AA.
 ID CHIC_LYCES
 AC Q05538;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
 GN CHI9.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=CV. MONETMAKER;
 RX MEDLINE=94003061; PubMed=8400122;
 RA Daubash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
 RT "Molecular characterization of four chitinase cDNAs obtained from
 Cladosporium fulvum-infected tomato.";
 RL Plant Mol. Biol. 22:1017-1029(1993).
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
 CONTAINING FUNGAL PATHOGENS.
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
 N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
 CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
 CC -!- INDUCTION: BY FUNGAL INFECTION.
 CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
 CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
 CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
 HYDROLASES).
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z15140; CAA78845.1; -.
 CC PIR; S37344; S37344.
 DR HSP; P23951; 2BAA.
 DR InterPro: IPR001002; Chitin_bind.
 DR InterPro: IPR000726; Glyco_hydro_19.
 DR Pfam; PF00187; chitin_binding; 1.
 DR Pfam; PF00182; Glyco_hydro_19; 1.
 DR PRINTS; PR00451; CHITINBINDNG.
 DR ProDom; PD000574; Glyco_hydro_19; 1.
 DR ProDom; PD000609; Chitin_bind; 1.
 DR SMART; SM00270; ChbD1; 1.
 DR PROSITE; PS00026; CHITIN_BINDING; 1.
 DR PROSITE; PS00773; CHITINASE_19_1; 1.
 DR PROSITE; PS00774; CHITINASE_19_2; 1.
 KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
 KW Hydroxylation; Multigene family.


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FT SIGNAL 1 22
FT CHAIN 23 315
FT PROPEP 316 322
FT DOMAIN 23 64
FT DISULFID 25 40
FT DISULFID 34 46
FT DISULFID 39 53
FT DISULFID 58 62
FT MOD_RES 66 66
FT MOD_RES 68 68
SQ SEQUENCE 322 AA; 34345 MW; D13A9191AE8FC5A CRC64;

Query Match 70.7%; Score 1248.5; DB 1; Length 322;
Best Local Similarity 72.6%; Pred. No. 6.9e-87;
Matches 228; Conservative 25; Mismatches 46; Indels 15; Gaps 5;

QY 9 MAAFAVSAHAECQSQAGATPCNLCCKSGFGCTTSDYCGTG-CQSOCCNGCSGGTP 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LLFSVLLLSASAEQCSQAGGALCASGLCCSKFGWCGTNEYCGPGNCQSQCPG----- 64

QY 68 VVPVTPSG--CGVSSIIISQSLFDOMLLHRNDAACLAK-GFVNYGAFVAAANSFSEATTG 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 --GPEPSGDLGV---ISNSMEDQMLHRNDNACQGNNEFYSYNAFVTAAGFFGCTTG 119

QY 125 STDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCTPSSQWPCAPG 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 DITARKREIAFLAQTSHETTGWPTAPDGPYAGWYCFLEQSGPDGYCTPSSQWPCAPG 179

QY 185 KKYFGRGPQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPS 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 KKYFGRGPQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPS 239

QY 245 HDVTGTWSPGDAQAGRVPGYVITNGLGECGSGDGRVADRIGFYKRYCDLIGV 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 HDVTGTWSPGDAQAGRVPGYVITNGLGECGSGDGRVADRIGFYKRYCDLIGV 299

QY 305 SYGNLDCYNORPF 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 SPGENLDCGNORSF 313
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RESULT 9
CH12_SOLTU STANDARD; PRT; 316 AA.
AC P52404;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTB2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
   and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
   CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
   N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
   SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
   SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
   OLD ROOT SEGMENTS, AND CARPELS.
```

```
CC -!- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U02606; AAA17408.1; -.
CC HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SMO0270; ChIBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
FT NON_TER 1
FT SIGNAL <1
FT CHAIN 19 309
FT PROPEP 310 316
FT DOMAIN 19 60
FT DISULFID 21 36
FT DISULFID 30 42
FT DISULFID 35 49
FT DISULFID 54 58
SQ SEQUENCE 316 AA; 33629 MW; 81FB3DB3F222A0C6 CRC64;

Query Match 70.3%; Score 1240.5; DB 1; Length 316;
Best Local Similarity 70.8%; Pred. No. 2.7e-86;
Matches 221; Conservative 31; Mismatches 47; Indels 13; Gaps 4;

QY 9 MAAFAVSAHAECQSQAGATPCNLCCKSGFGCTTSDYCGTG-CQSOCCNGCSGGTP 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LLFSVLLLSASAEQCSQAGGALCASGLCCSKFGWCGTNEYCGPGNCQSQ---CPGSP 63

QY 68 VVPVTPSGGVSSIIISQSLFDOMLLHRNDAACLAKG-FYNYGAFVAAANSFSEATTG 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 -----GDLGGVISNSMFDQMLHRNDNACQGNFYSYNAFISAAGSPFGFTGDI 115

QY 127 DYKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCTPSSQWPCAPGK 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 TARKREIAFLAQTSHETTGWPTAPDGPYAGWYCFLEQSGPDGYCTPSSQWPCAPGRK 175

QY 187 YFGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPSHD 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 YFGRGPIQISHNHYNGPAGQAIGTDLNPNPDLVADATVSFKTALWFMTPOSPKPSHD 235

QY 247 VITGRWSPGDAQAGRVPGYVITNGLGECGSGDGRVADRIGFYKRYCDLIGVSY 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 VITGRWSPGDAQAGRVPGYVITNGLGECGSGDGRVADRIGFYKRYCDLIGVSP 295

QY 307 GDNLDYCNORPF 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 GDNLDYCNORSF 307

RESULT 10
CH1X_PEA STANDARD; PRT; 320 AA.
ID CH1X_PEA
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QY 303 GYSYGNLDYCNORPF 318
DB 304 GVTGPNLDYCNORWF 319
RESULT 13
CH13_TOBAC
ID CH13_TOBAC STANDARD; PRT; 334 AA.
AC P29059;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14).
GN CHN14.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAVANA 425; TISSUE=Leaf;
RX MEDLINE=92269767; PubMed=1598915;
RA van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;
RT "The structure and regulation of homeologous tobacco endochitinase
genes of Nicotiana sylvestris and N. tomentosiformis origin.";
RL Mol. Genet. 232:460-469(1992).
CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS (PROBABLE).
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X64518; CAA45821.1; -.
CC PIR; S20982; S20982.
CC HSP; P27275; IMMC.
CC InterPro; IPR001002; Chitin_bind.
CC InterPro; IPR000726; Glyco_hydro_19.
CC Pfam; PF00187; Chitin_binding; 1.
CC Pfam; PF00182; Glyco_hydro_19; 1.
CC PRINTS; PR00451; CHITINBDNG.
CC ProDom; PD000574; Glyco_hydro_19; 1.
CC ProDom; PD000609; Chitin_bind; 1.
CC SMART; SM00270; ChtBD1; 1.
CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC PROSITE; PS00773; CHITINASE_19_1; 1.
CC PROSITE; PS00774; CHITINASE_19_2; 1.
CC Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
CC Hydroxylation; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 327 ENDOCHITINASE 3.
FT PROPEP 328 334 REMOVED IN MATURE FORM (PROBABLE).
FT DOMAIN 24 65 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 26 41 BY SIMILARITY.
FT DISULFID 35 47 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 59 63 BY SIMILARITY.
FT MOD_RES 67 67 HYDROXYLATION (POTENTIAL).
FT MOD_RES 69 69 HYDROXYLATION (POTENTIAL).
FT SEQUENCE 334 AA; 36220 MW; 4F684CE1FBD432FB CRC64;

Query Match 68.3%; Score 1206; DB 1; Length 334;
Best Local Similarity 67.9%; Pred. No. 1.le-83;
Matches 214; Conservative 32; Mismatches 65; Indels 4; Gaps 2;

QY 8 AMLAAFAVSAHAECGSGAGGATCPNCLCCSKFQFCGTTSDYCGTGC-QSQCNCGSGGT 66
DB 11 SLILVLELLLAVSAREQCGKQAGGARGCPGSMCCSNFGWCGNTQDYCGPGKQSQCPSPGPT 70
QY 67 ---PVPVTPSGGGVSSIIISQSLFDQMLHRNDAACLAAGFYNYGAFVAAANSFSGFAT 123
DB 71 PRPPTPTPGFTGDISIISSMFDQMLKRNNTQCGKSFYTYNAFITAAKSEFRGFT 130
QY 124 GSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP 183
DB 131 GDTTRKREVAFAAQTSHTTGGWTPADPGYAWGYCYLREGQNPSPCYVSSQWPCAP 190
QY 184 GKYPGGRGPIQISHNNYNYGPAQAIGTDLNPNPDLVASDATVSFKTALFWMTWTPSPKPS 243
DB 191 GKYYGGRGPIQISYNNYNYGPGRAIGQNLNPNPDLVATNAVVSFKSAIWFMTAQSPKPS 250
QY 244 SHDVTGRWSPSGADQAGRVPGYGVITNLINGLGLCGRGQDGRVADRIGFYKRYCDLIG 303
DB 251 CHDVTIGRWTPPSAADRAANKRLPGYGVITNLINGLGLCGHSDARVODRIGFYRRYCSILG 310
QY 304 VSYGDNLDYCNORPF 318
DB 311 VSPGDNIDCGNQKSF 325

RESULT 14
CH14_SOLTU
ID CH14_SOLTU STANDARD; PRT; 302 AA.
AC P52406;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ENDOCHITINASE 4 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
GN CHTB4.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DATURA; TISSUE=Leaf;
RX MEDLINE=94154255; PubMed=8111037;
RA Beerhues L., Kombrink E.;
RT "Primary structure and expression of mRNAs encoding basic chitinase
and 1,3-beta-glucanase in potato.";
RL Plant Mol. Biol. 24:353-367(1994).
CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
CC N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
CC -1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNG OF INTERMEDIATE AGE
CC SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
CC SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
CC OLD ROOT SEGMENTS, AND CARPELS.
CC -1- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
CC
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```

CC CC -! N-ACETYL-D-GLUCOSAMINE POLYMERS OF THE 1,4-BETA-LINKAGES OF
CC CC -! SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC CC HYDROLASES).
CC CC -----
CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC ENBL; M95835; AAA32986.1; -.
CC CC HSSP; P23951; 2BAA.
CC CC InterPro; IPR001002; Chitin_bind.
CC CC InterPro; IPR000726; Glyco_hydro_19.
CC CC Pfam; PF00187; chitin_binding; 1.
CC CC Pfam; PF00182; Glyco_hydro_19; 1.
CC CC PRINTS; PR00451; CHITINEBIND.
CC CC ProDom; PD000574; Glyco_hydro_19; 1.
CC CC ProDom; PD000609; Chitin_bind; 1.
CC CC SMART; SM00270; ChtBD1; 1.
CC CC PROSITE; PS00026; CHITIN_BINDING; 1.
CC CC PROSITE; PS00773; CHITINASE_19.1; 1.
CC CC PROSITE; PS00774; CHITINASE_19.2; 1.
CC CC Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Multigene family.
KW SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 322 ENDOCHITINASE CH25.
FT DOMAIN 21 62 CHITIN-BINDING (BY SIMILARITY).
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 32 44 BY SIMILARITY.
FT DISULFID 37 51 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
FT SEQUENCE 322 AA; 34816 MW; E62EE4B1721DBCDC CRC64;
CC SO

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Search completed: May 3, 2002, 18:48:33
Job time: 917 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 3, 2002, 18:47:01 ; Search time 157.87 Seconds
(without alignments)
295.565 Million cell updates/sec

Title: US-09-534-229c-3
Perfect score: 1765
Sequence: 1 MRGVVVVMAAAFAVSAHA.....DLIGVSYGNDLDCYNQRPFA 319

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1696.5	96.1	320	10 Q41539	O41539 triticum ae
2	1675.5	94.9	318	10 Q9AXR9	Q9AXR9 secale cere
3	1597	90.5	320	10 Q9SQL3	Q9SQL3 poa pratens
4	1557	88.2	340	10 Q9SQL4	Q9SQL4 poa pratens
5	1421	80.5	321	10 Q9FRV1	Q9FRV1 secale cere
6	1359.5	77.0	323	10 Q42993	Q42993 oryza sativ
7	1352.5	76.6	320	10 Q42994	Q42994 oryza sativ
8	1317.5	74.6	340	10 Q43294	Q43294 oryza sativ
9	1305	73.9	326	10 P93680	P93680 persea amer
10	1291.5	73.2	332	10 Q42839	Q42839 hordeum vul
11	1279	72.5	333	10 Q42992	Q42992 oryza sativ
12	1274	72.2	322	10 Q42995	Q42995 oryza sativ
13	1272.5	72.1	319	10 Q40667	Q40667 oryza sativ
14	1260	71.4	328	10 Q41180	Q41180 nicotiana t
15	1256	71.2	325	10 Q9FS45	Q9FS45 vitis vinif
16	1253	71.0	324	10 Q9FEW1	Q9FEW1 nicotiana s
17	1239.5	70.2	318	10 Q38777	Q38777 allium sati
18	1237	70.1	320	10 Q9SDY6	Q9SDY6 glycine max
19	1236	70.0	335	10 Q42970	Q42970 oryza sativ

20	1208.5	68.5	312	10 Q9M7F5	Q9M7F5 arabis pari
21	1208.5	68.5	325	10 P93327	P93327 medicago tr
22	1207.5	68.4	327	10 P94084	P94084 medicago sa
23	1206	68.3	315	10 Q9FXL8	Q9FXL8 psophocarpa
24	1205.5	68.3	305	10 Q9M7H2	Q9M7H2 arabis drum
25	1203.5	68.2	302	10 Q38776	Q38776 allium sati
26	1203.5	68.0	316	10 Q42428	Q42428 castanea sa
27	1198.5	67.9	329	10 O81145	O81145 solanum tub
28	1194.5	67.7	326	10 Q9M7H0	Q9M7H0 arabis fecu
29	1190.5	67.5	335	10 Q9S7J5	Q9S7J5 arabidopsis
30	1190.5	67.5	335	10 Q9S838	Q9S838 arabidopsis
31	1189.5	67.4	308	10 Q9M7H4	Q9M7H4 arabis blep
32	1186.5	67.2	315	10 Q43179	Q43179 solanum tub
33	1186.5	67.2	335	10 Q9SXJ4	Q9SXJ4 arabidopsis
34	1185.5	67.2	302	10 Q9M7G4	Q9M7G4 arabis lem
35	1185.5	67.2	310	10 Q9M7G9	Q9M7G9 arabis glab
36	1185.5	67.2	335	10 Q9SXJ2	Q9SXJ2 arabidopsis
37	1185	67.1	320	10 Q9M7G7	Q9M7G7 arabis glab
38	1184.5	67.1	335	10 Q9SXJ3	Q9SXJ3 arabidopsis
39	1183.5	67.1	306	10 Q9M7G2	Q9M7G2 arabis lign
40	1181.5	66.9	311	10 Q9M7F4	Q9M7F4 arabis pari
41	1180	66.9	311	10 O80404	O80404 cucurbita m
42	1177	66.7	325	10 Q9ZFK4	Q9ZFK4 vitis vinif
43	1174.5	66.5	297	10 Q9FUR3	Q9FUR3 vigna sesqu
44	1171.5	66.4	328	10 Q9ZPI0	Q9ZPI0 cicer ariet
45	1167.5	66.1	329	10 O81144	O81144 solanum tub

ALIGNMENTS

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RESULT 1
Q41539
ID Q41539 PRELIMINARY; PRT; 320 AA.
AC Q41539;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR.
GN CHIA1 OR CHI.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CHINESE SPRING;
RA Liao Y.C., Kreuzaler F., Fischer R., Reisener H.J., Tiburzy R.;
RL Plant Sci. 103:177-187(1994).
DR EMBL; X76041; CAA53626.1; -.
DR HSSP; P23951; 2BAA.
DR Mendel; 1463; Triae; Chial; 1463.
DR InterPro; IPR001002; Chitin_bind.
DR Pfam; PF00187; chitin_binding; 1.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBp1; 1.
DR PROSITE; PS00774; CHITINASE_19.2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 320 ENDOCHITINASE.
SQ SEQUENCE 320 AA; 33602 MW; F258D9DD8EF65E0E CRC64;

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Query Match 96.1%; Score 1696.5; DB 10; Length 320;
Best Local Similarity 95.3%; Pred. No. 1.5e-141;
Matches 305; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

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QY 1 MRGVVVVAMLAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
DB 1 MRGVVVVAMLAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
QY 61 GCSGGTVPVPTPGGGVSSIISSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFSG 119
DB 61 GCSGGTVPVPTPGGGVSSIISSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFSG 120
QY 120 FATGTGDKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCTPSSQW 179
DB 121 FATGTGADYKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGAASDYCSPNSQW 180
QY 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVASDATVSFKTALFWFWMTPOS 239
DB 181 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVASDATVSFKTALFWFWMTPOS 240
QY 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
DB 241 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 300
QY 300 DLGVSYGNDLDCYNORPFA 319
DB 301 DLGVSYGNDLDCYNORPFA 320
RESULT 2
Q9AXR9 PRELIMINARY; PRT; 318 AA.
ID Q9AXR9 AC Q9AXR9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000966; RA04454.1; -.
DR HSSP; P23951; ZBA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINIS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 318 AA; 33636 MW; BA685E1DB7A58B63 CRC64;
POTENTIAL.
FT SIGNAL.
KW Signal.
SQ SEQUENCE 1 20
Query Match 94.9%; Score 1675.5; DB 10; Length 318;
Best Local Similarity 94.7%; Pred. No. 1.le-139;
Matches 302; Conservative 9; Mismatches 7; Indels 1; Gaps 1;
QY 1 MRGVVVVAMLAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
DB 1 MRGVVVVAMLAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
QY 61 GCSGGTVPVPTPGGGVSSIISSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFSG 120
DB 61 RC-GGTPVPVPTPGGGVSSIISSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFSAF 119
QY 121 ATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCTPSSQWP 180
DB 120 ATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGAPSDYCSPPSQWP 179
QY 181 CAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVASDATVSFKTALFWFWMTPOS 240
DB 180 CAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVASDATVSFKTALFWFWMTPOS 239
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QY 241 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 300
DB 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDARVADRIGFYKRYC 299
QY 301 LLGVSYGNDLDCYNORPFA 319
DB 300 LLGVSYGNDLDCYNORPFA 318
RESULT 3
Q9SQL3 PRELIMINARY; PRT; 320 AA.
ID Q9SQL3 AC Q9SQL3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHITINASE.
GN CH12.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000966; RA04454.1; -.
DR HSSP; P23951; ZBA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINIS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 320 AA; 33711 MW; BEFC3ADBFE939B5 CRC64;
Query Match 90.5%; Score 1597; DB 10; Length 320;
Best Local Similarity 90.3%; Pred. No. 8.8e-133;
Matches 288; Conservative 15; Mismatches 14; Indels 2; Gaps 2;
QY 1 MRGVVVVAMLAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
DB 1 MRGLVVVITLVAFAVSAHAECGQAGGATCPNCLCCSKFGCGTTSYDTCGTGCSQCN 60
QY 61 GCSGGTVPVPTPS-GGGVSSIISSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFSG 119
DB 61 GCSGGTVPV-TPTSGGGGVSSIVSQSLFQDMLLRNDACLAAGFYNYGAFVAAANSFAG 119
QY 120 FATGTGDKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCTPSSQW 179
DB 120 FGTGTGTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYCFNQRGATSDYCSPPSQW 179
QY 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVASDATVSFKTALFWFWMTPOS 239
DB 180 PCAPGKKYFGRGPIQISHNYNYPAGQAGTDLNNPDIVATDPTVSFKTALFWFWMTAQ 239
QY 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
DB 240 KPSSHVDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDNRVADRIGFYKRYC 299
QY 300 DLGVSYGNDLDCYNORPFA 318
DB 300 DLGVSYGNDLDCYSQRPFA 318
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RESULT 4
Q9SQL4 PRELIMINARY; PRT; 340 AA.
AC Q9SQL4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CHITINASE.
GN Chil.
OS Poa pratensis (Kentucky bluegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Peaeae; Poa
OX NCBI_TaxID=4545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLADE;
RA Du M., Ha S.B.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000964; AAF04453.1; -
DR HSSP; P23951; 2BAA.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChIBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 340 AA; 36011 MW; 3613D7059A871E94 CRC64;

Query Match 88.2%; Score 1557; DB 10; Length 340;
Best Local Similarity 87.9%; Pred. No. 3.1e-129;
Matches 282; Conservative 17; Mismatches 18; Indels 4; Gaps 3;

QY 1 MRGVVVVAMLAFAVSAHAECGSGQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60
DB 1 MRGLVVVAILVAFAVSAHAECGSGQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60

QY 61 GCGSGTVPVPTPS-GGGVSSITISQSLFDQMLLRNDAAACLAGFYNYCAFVAANSEFG 119
DB 61 GCGSGTVPV-TPTPSGGGGVSSIVSRLFDRLHRNDGCAQAKGYTYDAFVAAGAF 119

QY 120 FATGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYNQERGATSDYCTPSSOW 179
DB 120 FGTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYNQERGATSDYCTPSSOW 179

QY 180 PCAPGKKGKRGPIQISHNINYGPAGQATGTDLLNPDVLVADATVSEKTALEFWMTQS 239
DB 180 PCAPGKKGKRGPIQISFNINYGPAGQATGTDLLNPDVLVADATVSEKTALEFWMTQS 239

QY 240 KPSSHDVITGRWSPSGADQAGRPVGYVITNIINGGLECGRGQDGR--VADRIGFYKR 297
DB 240 KPSSHDVITGRWSPSGADQAGRPVGYVITNIINGGLECGRGQDGR--VADRIGFYKR 297

QY 298 YCDLLGVSYGDNLDYCNQRPFF 318
DB 298 YCDLLGVSYGDNLDYCNQRPFF 320

RESULT 5
Q9FRV1 PRELIMINARY; PRT; 321 AA.
AC Q9FRV1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
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DE SEED CHITINASE-A.
GN RSCA.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohnuma T., Yamagami T., Ishiguro M.;
RT "Cloning and Sequencing of the Rye Seed Chitinase.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051578; BAB18519.1; -
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChIBD1; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 321 AA; 33641 MW; 76E5902BEC337C8E CRC64;

Query Match 80.5%; Score 1421; DB 10; Length 321;
Best Local Similarity 78.9%; Pred. No. 2.8e-117;
Matches 254; Conservative 29; Mismatches 35; Indels 4; Gaps 4;

QY 1 MRGVVVVAMLAFAVSAHAECGSGQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCN 60
DB 1 MGAFAFAVLAFAVSAHAECGSGQAGATCPNCLCCSKFGCGTTSYDYGTCGQSQCA 59

QY 61 GC-SGGTVP-PVPTPS-GGGVSSITISQSLFDQMLLRNDAAACLAGFYNYCAFVAANSEF 117
DB 60 GCGGGTPTPTPTPSGGGGVSSIVSRLFDRLHRNDGCAQAKGYTYDAFVAAGAF 119

QY 118 SGFATTGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGYNQERGATSDYCTPSS 177
DB 120 PFGFTGSTDVKKREVAFLAQTSHETTGWPTAPDGAFAFGYCFKQERGATSNCTPSA 179

QY 178 QWPCAPGKKGKRGPIQISHNINYGPAGQATGTDLLNPDVLVADATVSEKTALEFWMT 237
DB 180 QWPCAPGKKGKRGPIQISHNINYGPAGRAIGVDLLRNPDLVATDTVSFKTAMFWMTA 239

QY 238 QSPKPSHDVITGRWSPSGADQAGRPVGYVITNIINGGLECGRGQDGRVADRIGFYKR 297
DB 240 QAPKPSHAVITGQWSPSGTDRAGRPVGFVITNIVNGGIECGHGQDSRVADRIGFYKR 299

QY 298 YCDLLGVSYGDNLDYCNQRPFA 319
DB 300 YCDLLRVGYGNLDYCNQRPFA 321

RESULT 6
Q42993 PRELIMINARY; PRT; 323 AA.
AC Q42993; Q42996;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-
DE POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIA1 OR CHT-1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
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OC Eubryotidae: Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPONICA, CV. NIPPONBARE;
RX MEDLINE=94049667; PubMed=7901749;
RA Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
RT "Sequence variation, differential expression and chromosomal location
of rice chitinase genes";
RL Mol. Gen. Genet. 241:1-10(1993).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL: X56787; CAA40107.1; -
DR EMBL: D16222; BAA03750.1; -
DR HSP: P23951; 2BAA.
DR Mendel; 727; Oryza.Chial; 727.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtdB1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR Chitin-binding; Glycosidase; Hydrolase; Signal.
KW SIGNAL
FT CHAIN 33 340
FT CHAIN 33 340 CHITINASE.
SQ SEQUENCE 340 AA; 35586 MW; 642F13E3928CA7BE CRC64;

Query Match 74.6%; Score 1317.5; DB 10; Length 340;
Best Local Similarity 72.4%; Pred. No. 3.8e-108;
Matches 228; Conservative 36; Mismatches 50; Indels 1; Gaps 1;

QY 4 VYVAMIAAFVSAHAECQSGAGGATCPCNLCCKSGFCGTTSDYCTGCGSQCGSCG 63
DB 16 LVALLAVLAALATAARAECQAAGGARGPCNLCCKSGWCGTSDFCGCGSQCGSCG- 74
QY 64 GGTVPVPTPSGGVSSIIQSILFDMLLHRNDACLAKGFYNYGAFVAAANSFSGFAT 123
DB 75 GGTPTPTPSDPSGVSIPIRFLERLLHRNDGACPARGFYTYEAFLLAAAFAPFGGT 134
QY 124 GSTDKKREVAFLAQTSHETGGWFTAPDGPXSWGCFNQRGATSDYCTPSSOWPCAP 183
DB 135 GNETKREVAFLGQTSHETGGWFTAPDGPXSWGCFNQRGATSDYCTPSSOWPCAP 194
QY 184 GKXFGGPTQISHNYNYGPAQAIGTDLNNDPLVASDATVSKTALFWMTPOSPKPS 243
DB 195 GRKYYGKPTQISFNENYGPAGRAIGYDILLNNDPLVATDATVSKTALFWMTPOGKPS 254
QY 244 SHDVIITGRWSPSGADQAGRVPGYGVITNIINGLEGCGGQDGRVADRIGFYKRYCDLLG 303
DB 255 SHDVIITGRWSPSGADQAGRVPGYGVITNIINGLEGCGGQDGRVADRIGFYKRYCGAFG 314
QY 304 VSYGDNLDYCNQRP 318
DB 315 IGTTGNLDYCNQRP 329
ID P93680 PRELIMINARY; PRT; 326 AA.
AC P93680;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
GN CHIA1 OR CH11.
OS Persea americana (Avocado).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
OX NCBI_TaxID=3435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HASS; TISSUE=MESOCARP;
RA Sowka S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
RA Peterbauer C., Scheiner O., Breiteneder H.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z78202; CAB01591.1; -
DR HSP: P02877; 1HEV.
DR Mendel; 14766; Persea.Chial; 14766.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR ProDom; PD000574; Glyco_hydro_19; 1.
DR ProDom; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChtdB1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
DR Chitin-binding; Glycosidase; Hydrolase; Signal.
KW SIGNAL
FT CHAIN 26 326
FT CHAIN 26 326 ENDOCHITINASE.
SQ SEQUENCE 326 AA; 34586 MW; 643B20589E062E61 CRC64;

Query Match 73.9%; Score 1305; DB 10; Length 326;
Best Local Similarity 73.2%; Pred. No. 4.6e-107;
Matches 230; Conservative 35; Mismatches 41; Indels 8; Gaps 2;

QY 5 VYVAMIAAFVSAHAECQSGAGGATCPCNLCCKSGFCGTTSDYCTGCGSQCGSCG 64
DB 10 LLLLLVGLLAGEAFAECQSGAGGALCPGLCCSGFCGTTSDYCTGCGSQCGGV-- 67
QY 65 GTPVPVPTPSGGVSSIIQSILFDMLLHRNDACLAKGFYNYGAFVAAANSFSGFAT 124
DB 68 -TPSP-----GGVASLIQSIVFNQMLKRNDAQAKGFYNYAFIAANSFNGFASVG 121
QY 125 STDVKREVAFLAQTSHETGGWFTAPDGPXSWGCFNQRGATSDYCTPSSOWPCAP 184
DB 122 DTATRKREIAAFLAQTSHETGGWATAPDGPYAWGCFNQRGATSDYCTPSSOWPCAP 181
QY 185 KXFGGPTQISHNYNYGPAQAIGTDLNNDPLVASDATVSKTALFWMTPOSPKPS 244
DB 182 KXYGKPTQISYNYGPAQAIGYDILLNNDPLVATDPVISEKTLFWMTPOSPKPS 241
QY 245 HDVITGRWSPSGADQAGRVPGYGVITNIINGLEGCGGQDGRVADRIGFYKRYCDLLG 304
DB 242 HNVITGRWTPSADRAAGRLPGYGVITNIINGLEGCGKGFNDKVDADRIGFYKRYCDLLG 301
QY 305 SYGDNLDYCNQRP 318
DB 302 SYGDNLDYCNQRP 315
ID Q42839 PRELIMINARY; PRT; 332 AA.
AC Q42839;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-
DE ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
GN CHIA1 OR CHI33.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
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XX MEDLINE=96189256; PubMed=8605293;
RA Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
RT "Regulation, expression and function of a new basic chitinase gene in
PL rice (*Oryza sativa* L.);"
RL Plant Mol. Biol. 30:387-401(1996).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-
ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DR EMBL; X87109; CAAG60590.1; -;
DR HSSP; P23951; 2BAA.
DR Mendel; 1634; Oryza; Chial; 1634.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding; Glycosidase; Hydrolase; Signal.
PT SIGNAL 1 20
SQ SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;

Query Match 72.2%; Score 1274; DB 10; Length 322;
Best Local Similarity 70.8%; Pred. No. 2.4e-104;
Matches 233; Conservative 28; Mismatches 48; Indels 20; Gaps 4;
QY 1 MRGVVVVWVLAFAVSAHAECQSGAGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC- 59
DB 1 MRALAVVVVATAFAVAPQECGSGAGALCPNCLCCSQYGCWCGSTAYCGSGCQSQCS 60
QY 60 -----NGCGGGTVPVPTPSGGVSSIIQSFLDQMLLRNDAACLAKEFYNGAFV 111
DB 61 ROLRRRRDRPSSG-----GGSGVASIVSRSLFDQMLLRNDAACPAKLYIYDAFV 112
QY 112 AAANSFSGATGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGCYFNOERGAT-- 169
DB 113 AAANAFTTATGDAATRKREVAFLAQTSHETMTGWATAPDGPYSWGCYFKEENNGV 172
QY 170 SYCYCPSSOWPCAPGKKYGRGPIQISHNYNGPAGQATGTDLLNPNDLVADATVSFKT 229
DB 173 SDYCVQSSQWPCRAKKYGRGPIQISYNYNGPAGQATGNSLLNPNDL-ASDATVSFKT 231
QY 230 ALFWFMTQSPKPSHDVTGRWSPSGADQAGRVPGYGVITNIINGLECGRGQDGRVA 289
DB 232 AFWFMTQSPKPSCHAVTGWTPNGNDQAGRVPGYGVITNIINGVECGHGADSRVA 291
QY 290 DRIGFYKRYCDLGVSYGNDLCYNORPF 318
DB 292 DRIGFYKRYCDMLGVSYGANLDCYNORPF 320

RESULT 13
Q40667 PRELIMINARY; PRT; 319 AA.
AC Q40667;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CHITINASE CLASS I.
GN CHIAL.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoidaeae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y., Baek J., Park H., Choi Y., Kim S.;
RL Biosci. Biotechnol. Biochem. 0:0-0(1994).
DR EMBL; Z29961; CAAG2849.1; -;

DR HSSP; P23951; 2BAA.
DR Mendel; 1578; Oryza; Chial; 1578.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR PRODOM; PD000609; Chitin_bind; 1.
DR SMART; SM00270; ChitBD1; 1.
DR PROSITE; PS00773; CHITINASE_19_1; 1.
DR PROSITE; PS00774; CHITINASE_19_2; 1.
DR PROSITE; PS00026; CHITIN_BINDING; 1.
KW Chitin-binding.
SQ SEQUENCE 319 AA; 33600 MW; C990572C114FC0A9 CRC64;

Query Match 72.1%; Score 1272.5; DB 10; Length 319;
Best Local Similarity 73.0%; Pred. No. 3.3e-104;
Matches 235; Conservative 29; Mismatches 49; Indels 9; Gaps 5;
QY 1 MRGVVVVWVLAFAVSAHAECQSGAGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
DB 1 MRALAVVVVATRFVAVVPPQCGSGAGALCPNCLCCSQYGCWCGSTAYCGSGCQSQCS 60
QY 61 GCGSGTVPVPTPSGG--GVSSIIQSFLDQMLLRNDAACLAKEFYNGAFVAAANSFS 118
DB 61 GCGGGGADPA---SGGASGVASIVSRSLFDQMLLRNDAACPAKNFYTYDAFVAANAYP 117
QY 119 GFATGSTDVKKREVAFLAQTSHETTGWPTAPDGPYSWGCYFNOERGAT--SDYCTPS 176
DB 118 DFATGDAATRKREVAFLAQTSHETTGWATAPDGPYSWGCYFKEENNGVSDYCYQS 177
QY 177 SOWCAPGKKYGRGPIQISHNYNGPAGQATGTDLLNPNDLVADATVSFKTALFWMT 236
DB 178 SQCRCA-GKKYGRGPIQISYNYNGPAGQATGNSLLNPNDLVADAT-LSFKTAFWFMT 235
QY 237 POSKPSSHDVTGRWSPSGADQAGRVPGYGVITNIINGLECGRGQDGRVADRIGFYK 296
DB 236 POSKPSCHAVTGWTPNGNDQAGRVPGYGVITNIINGVECGHGADSRVADRIGFYK 295
QY 297 RYCDLGVSYGNDLCYNORPF 318
DB 296 RYCDMLGVSYGANLDCYNORPF 317

RESULT 14
Q41180 PRELIMINARY; PRT; 328 AA.
AC Q41180;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BASIC CHITINASE.
GN CHIAL.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9240740; PubMed=2152343;
RA Neale A.D., Wahlethner J.A., Lund M., Bonnett H.T., Kelly A.,
RA Meeks-Wagner D.R., Peacock W.J., Dennis E.S.;
RT "Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in
tobacco explants during flower formation.";
RL Plant Cell 2:673-684(1990).
DR EMBL; S44869; AAB23374.1; -;
DR HSSP; P23951; 2BAA.
DR Mendel; 14770; Nicotiana; Chial; 14770.
DR InterPro; IPR001002; Chitin_bind.
DR InterPro; IPR000726; Glyco_hydro_19.

DR	Ffam:	PF00187;	chitin_binding;	1.
DR	Pfam:	PF00182;	Glyco_hydro_19;	1.
DR	PRINTS:	PR00451;	CHITINBINDNG.	
DR	ProDom:	PD000574;	Glyco_hydro_19;	1.
DR	ProbDom:	PD000609;	Chitin_bind;	1.
DR	SMART:	SM00270;	ChtBDP1.	1.
DR	PROSITE:	PS00773;	CHITINASE_19;	1.
DR	PROSITE:	PS00774;	CHITINASE_19_2;	1.
DR	PROSITE:	PS00026;	CHITIN_BINDING;	1.
KW	Chitin-binding.			
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Best Local Similarity 71.8%; Pred.No. 4.3e-103;				
Matches 224; Conservative 31; Mismatches 53; Indels 4; Gaps				
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QY	127	DVKREVAAPLACTSHETTGMPAPTADGPYSWGVCFNQBRGATSDYCTPSSQWPACPKK	186	
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QY	187	YFGRGPIQTISHNNYGPAQAIGTDLLNPNPLVASDATVSFTALWFMTPOSPKPSSH	246	
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QY	247	VITGRVSPGCAAGRVPGYGVITIINGGLECRGDGRVADRIGFYKRYCDLLGVSY	306	
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RESULT 15
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AC Q9FS45;
DT 01-MAR-2001 (trEMBLrel. 16, Created)
DT 01-MAR-2001 (trEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (trEMBLrel. 17, Last annotation update)
DE CHITINASE PRECURSOR (EC 3.2.1.14).
GN CHITIB.
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=29760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Ugni Blanc; TISSUE=LEAF;
RA Robert N., Roche K., Lebeau Y., Breda C., Boulay M., Esnault R.,
RA Buffard D.;
RT "Molecular characterization of Vitis vinifera genes encoding
RT chitinases differentially expressed in berries and leaves infected by
RT fungal or bacterial pathogens.";
KL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ291506; CAC14015.1; -.
DR InterPro: IPR001002; Chitin_bind.
DR InterPro: IPR000726; Glyco_hydro_19.
DR Pfam; PF00187; Chitin_binding; 1.
DR Pfam; PF00182; Glyco_hydro_19; 1.
DR PRINTS; PR00451; CHITINBINDNG.
DR PRODOM; PD000574; Glyco_hydro_19; 1.
DR SMART; SMC0270; ChitBD1; 1.

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:21:51 ; Search time 3990.51 Seconds
(without alignments)
3187.393 Million cell updates/sec

Title: US-09-534-229c-6

Perfect score: 771

Sequence: 1 atggcgaggttgctgcctc.....agaggacttcgtagctag 771

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_om.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_sy.*

28: em_un.*

29: em_vi.*

30: em_htgo_hum.*

31: em_htgo_inv.*

32: em_htgo_rod.*

33: em_htg_hum.*

34: em_htg_inv.*

35: em_htg_rod.*

36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Match	Length	DB	ID	Description
1	711.8	92.3	1028	8	HVCHT2A	X78671 H.vulgare m
2	659	85.5	1013	8	HVCHT2B	X78672 H.vulgare m
3	654.2	84.9	998	8	AF280438	AF280438 Secale ce
4	636.8	82.6	890	8	HVU276226	AJ276226 Hordeum v
5	559.6	72.6	923	8	ABU16497	ABU16497 Oryza sat
6	474.4	61.5	913	8	OSAF001500	AF001500 Oryza sat
7	395.2	51.3	652	8	RICRCH0	L40338 Oryza sativ
8	329.6	42.7	1186	8	OSLMRNAC	X56787 O.sativa L.
9	307.2	39.7	1291	8	RICCHITA	L37289 Oryza sativ
10	302.8	39.3	1173	8	AF000965	AF000965 Poa prate
11	302.2	39.2	1080	8	AF000966	AF000966 Poa prate
12	301.4	39.1	1985	8	TACHIG	X76041 T.aestivum
13	300.6	39.0	1151	6	I84465	I84465 Sequence 2
14	296.2	38.4	2808	8	RICCHT3	D16223 Rice Cht-3
15	296.2	38.4	141534	2	AP003685	AP003685 Oryza sat
16	296	38.4	1779	8	BLXCHI33A	L34211 Hordeum vul
17	295.6	38.3	998	8	BLXCHI	M62904 H.vulgare L
18	295.6	38.3	1002	6	A37990	A37990 Sequence 9
19	295.6	38.3	1002	6	AR037574	AR037574 Sequence 9
20	295.6	38.3	1002	6	I75200	I75200 Sequence 9
21	295.6	38.3	3169	8	BLXCHI26A	L34210 Hordeum vul
22	294.6	38.2	1192	8	AF280437	AF280437 Secale ce
23	291.8	37.8	1018	8	AB051579	AB051579 Secale ce
24	283.6	36.8	1252	8	AF000964	AF000964 Poa prate
25	279.6	36.3	138825	8	AC051633	AC051633 Oryza sat
26	278.4	36.1	1160	8	OSENDO	X56063 O.sativa mR
27	277.8	36.1	2739	8	RICCHT1	D16221 Rice Cht-1
28	277.8	36.0	1191	8	AB051578	AB051578 Secale ce
29	277.8	36.0	1684	8	HVU02287	U02287 Hordeum vul
30	273.2	35.4	1051	8	OSU02286	U02286 Oryza sativ
31	269	34.9	1237	8	OSCHIT	X54367 Oryza sativ
32	266.2	34.5	1159	8	OSCHITIA	Z29961 O.sativa (P
33	262.2	34.0	1300	8	AB012855	AB012855 Oryza sat
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36	260.4	33.8	2048	8	OSDNARC24	X87109 O.sativa RC
37	239.6	31.1	1005	8	TOBPRQ	M29868 Tobacco pat
38	239.6	31.1	1020	6	AR016782	AR016782 Sequence
39	239.6	31.1	1020	6	AR020808	AR020808 Sequence
40	239.6	31.1	1020	6	AR027131	AR027131 Sequence
41	239.6	31.1	1020	6	AR038418	AR038418 Sequence
42	239.6	31.1	1020	6	AR064560	AR064560 Sequence
43	239.6	31.1	1020	6	AR067485	AR067485 Sequence
44	239.6	31.1	1020	6	I07381	I07381 Sequence 31
45	239.6	31.1	1020	6	I38437	I38437 Sequence 7

ALIGNMENTS

RESULT	1					
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LOCUS	HVCHT2A	1028 bp	mRNA	PLN	01-NOV-1994	
DEFINITION	H.vulgare mRNA for chitinase 2a.					
ACCESSION	X78671					
VERSION	X78671.1	GI:563486				
KEYWORDS	chitinase.					
SOURCE	barley.					
ORGANISM	Hordeum vulgare					
REFERENCE	1 (bases 1 to 1028)					
AUTHORS	Bryngelsson, T., Collinge, D.B., Green, B., Gunnesson, P.O., Kragh, K. and Thordal-Christensen, H.					
TITLE	Purification, characterization and cDNA sequence of a basic chitinase from barely infected with powdery mildew					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 1028)					
AUTHORS	Bryngelsson, T.L.					


```

TITLE      Direct Submission
JOURNAL    Submitted (16-MAR-1994) T.L. Bryngelsson, Department of Plant
           Breeding Research, The Swedish University of Agricultural Sciences,
           S-268 31 Svaloev, SWEDEN
FEATURES   Location/Qualifiers
source     1..1028
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           /cultivar="Pallas, near-isogenic line p02"
           /db_xref="taxon:4513"
           /dev_stage="seedling"
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           /size=829
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Best Local Similarity 95.2%; Pred. No. 9.4e-88;
Matches 734; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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QY 61 ggggttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
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Db 119 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 178
QY 121 ctgcccacccgcgacactcgtgtgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
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Db 179 CTGCCCAACCGGACAACTCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 238
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QY 241 cgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
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Db 359 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418
QY 361 ccaccatactatgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 420
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Db 539 GGTCTCTTCAGGACGGCGATGTGGTTCCTGGATACGCGCGCGGCAACAGCGCTCGAGC 598
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QY 601 ccggatcaggagtgatcaccaatcatcatcaacggcgggcgcgcgcgcgcgcgcgcgc 660
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RESULT      2
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DEFINITION  H.vulgare mRNA for chitinase 2b.
ACCESSION   X78672
VERSION     X78672.1 GI:563488
KEYWORDS    chitinase.
SOURCE      barley.
ORGANISM    Hordeum vulgare
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Hordeum.
            1 (bases 1 to 1013)
            Bryngelsson,T., Collinge,D.B., Green,B., Gummesson,P.O., Kragh,K.
            and Thordal-Christensen,H.
            Purification, characterization and cDNA sequence of a basic
            chitinase from barely infected with powdery mildew
            Unpublished
            2 (bases 1 to 1013)
            Bryngelsson,T.L.
            Direct Submission
            Submitted (16-MAR-1994) T.L. Bryngelsson, Department of Plant
            Breeding Research, The Swedish University of Agricultural Sciences,
            S-268 31 Svaloev, SWEDEN
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[illegible]

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 Db 967 GCGCGCGGGGAGGGTGCCCGGGGTACGGCGGTGATCATTAAATCATCAACGCGCGGCTCGA 1026
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 Db 1027 GTGCGGCAAGGGGAGGACACACCGCGTCGCGGACAGGATCGGGTTCTACAAGCGCTACTG 1086
 QY 705 cggcgatgctcggcacggcgcaaccgagggaggaacactgcactgcctacaccagaggaaactcgc 764
 Db 1087 CGACCTCTCGGCGTGAGCTTACGGGGACACCTGGACTGCTACACGAGAGCGCGTCAA 1146
 QY 765 tagcta 770
 Db 1147 TGGTTA 1152

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 DEFINITION Poa pratensis chitinase (Chi2) gene, complete cds.
 ACCESSION AF000966
 VERSION AF000966.1 GI:6164587
 KEYWORDS
 SOURCE Kentucky bluegrass.
 ORGANISM Poa pratensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidaeae; Poae; Poa.
 1 (bases 1 to 1080)
 Du.M. and Ha.S.B.
 Direct Submission
 Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, CA
 94706, USA

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LOCUS       AP003685      141534 bp            DTG       24-MAY-2001
DEFINITION  Oryza sativa chromosome 6 clone P0548E04, *** SEQUENCING IN
PROGRESS   ***, in ordered pieces.
ACCESSION  AP003685
VERSION    AP003685
KEYWORDS   HTG; HTGS,PHASE2
SOURCE     Oryza sativa (cultivar:Nipponbare) DNA, clone:P0548E04.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
1 (sites)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0548E04
2 Published Only in DataBase (2001) In press
2 (bases 1 to 141534)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (23-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kanondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@agr.affrc.go.jp; URL:http://rgp.dna.affrc.go.jp/;
Tel.:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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QY	199	ttcccgggttcggcaaccaccgcgcgcgcgcacataaagcgcgcaccttcgcgcgttc	258					
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Db	19651	CTGGCGCAGAGTCCCACGAGACACCGCGCGTGTGCCACGCGCCCGCAGCGCCCCCTAC	19592					
QY	316	cagtggggtactgcttcagaagaagataaagcaaggccactcccca-----	363					
Db	19591	TCCTGGGGCTACTGCTTAAGGAGGAGAACAAGGCAACGCCGCCACATACTGGAGGCC	19532					
QY	364	-----ccatatgatgagcgggacccatcaattg	393					
Db	19531	AAGCGCGAGTGGCGGTGCGCGCGCGCAAGAGACTACTCGCGCGGGGGACCCATCCAGATC	19472					

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:36:06 ; Search time 309.71 Seconds
(without alignments)
2134.247 Million cell updates/sec

Title: US-09-534-229c-6
Perfect score: 771
Sequence: 1 atggcgagtttgcgcct.....agaggaacttgcgtagctag 771

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 segs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651.2	84.5	756	20	AA24890 Rye chitinase-like
2	470.6	61.0	1013	21	AA96231 cDNA encoding a ma
3	327.4	42.5	1077	21	AA96230 cDNA encoding a ma
4	300.6	39.0	1151	13	AAQ31408 RCH10 chitinase ge
5	300.6	39.0	1151	16	AAQ81346 Rice chitinase RCH
6	299.4	38.8	954	20	AA24889 Rye chitinase-like
7	297.4	38.6	3035	22	AAF54983 Nucleotide sequenc
8	295.5	38.3	1002	15	AAQ62518 Sequence encoding
9	262.2	34.0	1318	19	AAV49982 Floral organ-speci
10	246	31.9	1163	21	AA96224 cDNA encoding a ma
11	239.6	31.1	1010	11	AAQ06185 PR-Q cDNA cloned i

12	239.6	31.1	1020	10	AA90845 Tobacco PR-Q gene.
13	239.6	31.1	1020	20	AAV62809 Tobacco PR-Q gene
14	239.6	31.1	1020	20	AAV72995 PR-Q protein encod
15	235.4	30.5	965	12	AAQ12897 petunia extracellu
16	235.4	30.5	966	18	AA789951 petunia hybrida ex
17	235.4	30.5	966	21	AA58909 cDNA sequence enco
18	218.2	28.3	968	11	AAQ06186 PR-P cDNA cloned i
19	218.2	28.3	968	20	AAV62813 Tobacco PR-P gene
20	218.2	28.3	968	20	AAV62813 PR-P protein encod
21	213.2	27.7	4704	11	AAQ05264 cDNA encoding a ma
22	200.2	26.0	1118	21	AA96233 Chitinase coding s
23	199.6	25.9	879	18	AA77940 Full length chitin
24	199.6	25.9	996	18	AA77941 cDNA encoding a ma
25	198.6	25.8	583	21	AA96234 Banana ripening fr
26	196.4	25.5	7397	20	AA25613 Wild tomato endoch
27	193.4	25.1	966	16	AAQ93034 Wild tomato endoch
28	190.2	24.7	935	16	AAQ93035 American elm chiti
29	185	24.0	1225	17	AA73325 Tobacco intracellu
30	159	20.6	1152	12	AAQ12898 Nicotiana sp. intr
31	159	20.6	1152	18	AA789952 cDNA sequence enco
32	159	20.6	1152	21	AA58910 Banana fruit ripen
33	158.8	20.6	721	20	AAV69461 Floral organ-speci
34	153.8	19.9	2636	19	AAV49983 Sequence encoding
35	153.6	17.6	1153	13	AAQ21007 Endochitinase prec
36	135.6	17.6	1153	15	AAQ68352 Sequence of chimera
37	135.6	17.6	1160	13	AAQ21191 Sequence of chimera
38	135.6	17.6	1863	13	AAQ4261 Tomato-tobacco end
39	135.6	17.6	1863	15	AAQ4261 Potato infection i
40	129.6	16.8	501	21	AAA40411 Chitinase gene con
41	129.2	16.8	3850	12	AAQ11093 Basic chitinase ge
42	129.2	16.8	3850	12	AAQ15147 Banana fruit ripen
43	129	16.7	755	20	AAV69463 Rye chitinase-like
44	121.4	15.7	292	20	AA24892 cDNA encoding a ma
45	119.8	15.5	1048	21	AA96232

ALIGNMENTS

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ID	AA24890 standard; cDNA; 756 bp.
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AC	AA24890;
XX	
DT	21-JUN-1999 (first entry)
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DE	Rye chitinase-like protein CHT46 cDNA clone ch-46.
XX	
KW	CHT46; chitinase-like protein; antifreeze protein; AFP;
KW	winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW	transgenic plant; preservation; cryopreservation; tumour; therapy;
KW	ss.
XX	
OS	Secale cereale.
XX	
PH	Key
FT	CDS
FT	Location/Qualifiers
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FT	WO9906565-A2.
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PD	11-FEB-1999.
XX	
PF	31-JUL-1998; 98WO-CA00745.
XX	
PR	31-JUL-1997; 97US-0903872.

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:25:26 ; Search time 142.45 Seconds
(without alignments)
1225.795 Million cell updates/sec

Title: US-09-534-229C-6
Perfect score: 771
Sequence: 1 atgcgaggttgctgcct.....agaggaaactcgtagctag 771

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 11328999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	300.6	39.0	1151	1	Sequence 1, Appli
4	295.6	38.3	1002	1	Sequence 2, Appli
5	295.6	38.3	1002	1	Sequence 9, Appli
6	295.6	38.3	1002	1	Sequence 9, Appli
7	239.6	31.1	1020	1	Sequence 9, Appli
8	239.6	31.1	1020	1	Sequence 7, Appli
9	239.6	31.1	1020	1	Sequence 7, Appli
10	239.6	31.1	1020	1	Sequence 7, Appli
11	239.6	31.1	1020	1	Sequence 7, Appli
12	239.6	31.1	1020	1	Sequence 7, Appli
13	239.6	31.1	1020	1	Sequence 7, Appli
14	239.6	31.1	1020	1	Sequence 7, Appli
15	239.6	31.1	1020	2	Sequence 7, Appli
16	239.6	31.1	1020	2	Sequence 7, Appli
17	239.6	31.1	1020	2	Sequence 7, Appli
18	239.6	31.1	1020	2	Sequence 7, Appli
19	239.6	31.1	1020	2	Sequence 7, Appli
20	239.6	31.1	1020	4	Sequence 7, Appli
21	235.4	30.5	966	1	Sequence 7, Appli
22	235.4	30.5	966	3	Sequence 8, Appli
23	235.4	30.5	966	3	Sequence 8, Appli
24	218.2	28.3	968	1	Sequence 12, Appl
25	218.2	28.3	968	1	Sequence 12, Appl
26	218.2	28.3	968	1	Sequence 12, Appl
27	218.2	28.3	968	1	Sequence 12, Appl

28 218.2 28.3 968 1 US-08-456-265A-12 Sequence 12, Appli
29 218.2 28.3 968 1 US-08-455-416-12 Sequence 12, Appli
30 218.2 28.3 968 1 US-08-455-244-12 Sequence 12, Appli
31 218.2 28.3 968 1 US-08-454-876-12 Sequence 12, Appli
32 218.2 28.3 968 2 US-08-457-364-12 Sequence 12, Appli
33 218.2 28.3 968 2 US-08-456-262-12 Sequence 12, Appli
34 218.2 28.3 968 2 US-08-456-240-12 Sequence 12, Appli
35 218.2 28.3 968 2 US-08-455-736-12 Sequence 12, Appli
36 218.2 28.3 968 2 US-08-971-217-12 Sequence 12, Appli
37 218.2 28.3 968 4 US-09-350-600-12 Sequence 12, Appli
38 195 25.3 966 1 US-08-162-475A-1 Sequence 1, Appli
39 190.2 24.7 935 1 US-08-162-475A-3 Sequence 3, Appli
40 185 24.0 1225 1 US-08-286-020-1 Sequence 1, Appli
41 185 24.0 1225 2 US-08-603-919-1 Sequence 1, Appli
42 160.2 20.8 943 1 US-08-475-427-15 Sequence 15, Appli
43 160.2 20.8 943 2 US-07-842-165-15 Sequence 15, Appli
44 159 20.6 1152 1 US-08-047-413-10 Sequence 10, Appli
45 159 20.6 1152 3 US-08-229-050-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 39.0%; Score 300.6; DB 1; Length 1151;
Best Local Similarity 65.6%; Pred. No. 1.1e-51;
Matches 494; Conservative 0; Mismatches 214; Indels 45; Gaps 2;

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Db 636 TGAATATACCAATCATTAACGGTGAATTGAATGGCATAGGACGGAATGACGCAGT 695
QY 672 cftcgacgcgcatcggtactacacgcgtactcggtcggtcgatcggtcgacgcccacccggagg 731
Db 696 GGAAGATCGAATGGATACACTACAGAGGATATGCTGTATGTTAAATCTTGCTCCGGGGGA 755
QY 732 caactcgactgtacacccagagggaacttcg 763
Db 756 AAACCTGGACTGTACAAACCAAGAACTTCG 787

RESULT 8

US-08-449-315-7
; Sequence 7, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:

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Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9; Gaps 2;

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QY 372 tggacgggggacccatccaattgacagggcggtccaactacgatotttcgggagagcgat 431
Db 396 TGGTAGAGGAGCCCATCCCAATTGACAAACCGAAATTAACATATGAGAAAGCTGGAATGCAT 455
QY 432 cgggaaggacctggtgagcaacccagacactagtgctccacgacgcggtggtgtcctcag 491

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Db 165 GAACGACGGTAGATGCTGCTGCAATGGCTTCTACACTTATGATGCAITTCATAGCTGCTGC 224
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Qy 312 gtccagtggttgactctctcaaggaagataagaagccacgtccccacacatacta 371
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Qy 372 tggacggggaccatcccaattgacagggcggtcccaactacgatcttgcgggagagcgat 431
Db 396 TGGTAGAGGACCCATCCATTCGACAAACCGAATACATGAGAAAGCIGGAACCTGCAAT 455
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Qy 732 caacctgactgctacacccagaggaaactcgc 763
Db 756 AAACCTGGACTGTTACCAACCAAGAACTTCG 787

RESULT 13

US-08-455-244-7

Sequence 7, Application US/08455244

Patent No. 5789214

GENERAL INFORMATION:

APPLICANT: Ryals, John A.

APPLICANT: Alexander, Danny C.

APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.

APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian

APPLICANT: Meins, Jr., Frederick

APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc

APPLICANT: Payne, George B.

APPLICANT: Sperison, Christoph

APPLICANT: Stinson, Jeffrey R.

APPLICANT: Ukens, Scott J.

APPLICANT: Ward, Eric R.

APPLICANT: Williams, Sherioka C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 14:24:00 ; Search time 3076.35 Seconds
(without alignments)
2693.125 Million cell updates/sec

Title: US-09-534-229C-6

Perfect score: 771

Sequence: 1 atggcgaggttgctgcct.....agaggaacttcgctagtag 771

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estom:*
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8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661.6	85.8	906	11	BF065825 HV_CEB001
2	623.6	80.9	824	11	BF064990 HV_CEB002
3	597.6	77.5	937	10	BE559387 HV_CEB002
4	589.2	76.4	923	11	BF065694 HV_CEB001
5	569.2	73.9	829	11	BF065067 HV_CEB002
6	568.6	73.7	936	11	BF066058 HV_CEB001
7	562.4	72.9	842	11	BF264498 HV_CEB000
8	545.4	70.7	669	10	BE215473 HV_CEB000
9	538.6	69.9	695	10	BE214577 HV_CEB000
10	523.6	67.9	725	10	BE214283 HV_CEB000
11	511.6	66.4	713	11	BF628657 HVSMEB000
12	496	64.3	583	10	BE216024 HV_CEB000

13	495.4	64.3	923	10	BE559371 HV_CEB002
14	442.4	57.4	576	11	BF266125 HV_CEB001
15	434.2	56.3	568	11	BF265978 HV_CEB001
16	432.4	56.1	699	10	BE214483 HV_CEB000
17	425	55.1	541	11	BF257510 HVSMEF001
18	423	54.9	573	11	BF065377 HV_CEB001
19	420.4	54.5	509	10	BE587679 WHF0667_G
20	397.4	51.5	791	11	BF265236 HV_CEB001
21	396.8	51.5	789	11	BF621706 HVSMEB001
22	388.6	50.4	875	11	BF623602 HVSMEB000
23	387.2	50.2	466	10	BE586541 WHF0505_G
24	362.4	47.0	505	10	BE215793 HV_CEB000
25	355.6	46.1	457	10	BE420363 WNS05_G8R
26	346	44.9	753	11	BF259671 HVSMEF001
27	341.2	44.3	793	11	BF624096 HVSMEB000
28	337	43.7	628	10	BE493038 WHF0562_G
29	318.2	41.3	972	11	EG837392 Zml0_06h0
30	305.2	39.6	549	11	EG906960 TaLr1156A
31	286.6	37.2	1123	11	BF262973 HV_CEB000
32	278.8	36.2	805	11	EG365536 HVSMEB1000
33	255.4	33.1	954	11	BF265189 HV_CEB001
34	250	32.4	472	11	C72797 C72797 Rice
35	239.6	31.1	574	10	AW461042 707097F10
36	238.4	30.9	729	10	BE602672 HVSMEB010
37	237.8	30.8	681	10	BF705117 Sc02_08b0
38	236.2	30.6	912	11	EG301220 HVSMEB001
39	235.2	30.5	731	10	BE602548 HVSMEB009
40	233.6	30.3	742	11	EG365634 HVSMEB1000
41	229.2	29.7	525	10	AW927987 945003H06
42	228.4	29.6	808	11	EG837580 Zml0_02h0
43	227.8	29.5	503	10	BE055947 945020F07
44	226.4	29.4	806	11	EG414551 HVSMEB000
45	226.2	29.3	794	11	EG837630 Zml0_03a0

ALIGNMENTS

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RESULT 1
BF065825 906 bp mRNA 09-MAR-2001
LOCUS HV_CEB0014B14f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCNDA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
            HV_CEB0014B14f, mRNA sequence.
ACCESSION BF065825
VERSION BF065825.2 GI:13265390
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 906)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
            Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
            T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
            Wood,T.
TITLE Development of a genetically and physically anchored EST resource
            for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Oct 17, 2000 this sequence version replaced gi:10842464.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: AATTACCTCCTCACTAAGG
            High quality sequence stop: 749.
            Location/Qualifiers
                1..906
                /organism="Hordeum vulgare"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE AUTHORS

1 (bases 1 to 923)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.

TITLE

Development of a genetically and physically anchored EST resource
for barley genomics

JOURNAL COMMENT

Unpublished (2000)
On Oct 17, 2000 this sequence version replaced gi:10842333.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTACCCCTCACTAAAGG

High quality sequence stop: 640.

FEATURES source

1..923
/organism="Hordeum vulgare"
/cultivar="Cil16151 (M1a6)"
/db_xref="taxon:4513"
/clone="HV_CEB0013H08f"
library HVCDNA0005 (Erysiphe infected & control)
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders".
194 a 277 c 282 g 170 t

BASE COUNT ORIGIN

Query Match 76.43; Score 589.2; DB 11; Length 923;
Best Local Similarity 87.24; Pred. No. 9.5e-104;
Matches 670; Conservative 0; Mismatches 93; Indels 5; Gaps 2;

Qy 1 atggcgaggttgctgcctcgccgtgtgaccccgccctcctgctgcgcgtgcgcg 60
Db 42 ATGCGAGGCTGCTGCTCCCTGCGGTGTGCGCCCGCCCGCTCCCTGCTGCGCGCGGTG 101
Qy 61 gggggtgocggcgcgagggcggtggctgcgtatcatcagcggtggtgtagcgagcact 120
Db 102 GCGCGCGCGCGCGCAAGCGGTGGCTCGGTATCATCGCGGTGCGGTACGCGAGCATG 161
Qy 121 ctgcccacccgcgaactcgtgtgocggcgagaggttctacagtagcagccttc 180
Db 162 CTGCCCCAACCGCGACAACCTGCTGTGCCCGCCAGGGGGTTCATACGTACGACGCCCTC 221
Qy 181 atcgccgcgcgaacacaccttcccggttctggccaccacggcgagcgcgacataaag 240
Db 222 ATCGCGGAGCCACACACTTTCGGGCTTCGGCACCCAGCGCGCGCATCATCAAG 281
Qy 241 cgcgacctgcgccttcttcggccagacacctccacagagacacccggaggagagc 300
Db 282 CGCGAGCTCGCGCGCTTCTTCGGCCAGACCTCCACGAGACACCGGAGGAGCAGAGGC 341
Qy 301 gctaccacacgttccagtgggtactgcttcaaggagagataagcaaggcaagcctcc 360
Db 342 GCCCGGACAGTTCCTCAAGGGGCTACTGCTCAAGGAAGAGATAAGCAAGGCCACGCT 401
Qy 361 ccaccatactgagcgggggaccatccaatgtacagggcggttccactacgattctgcc 420
Db 402 CCACCTACTATGACGGGGACCCATCAATTGACAGGGCGGTCCACTAGATCTGCC 461
Qy 421 gggagagcgtcggaaggaacctggtgagcaaccacagaccttagtgcacggagcggtg 480
Db 462 GGGAGAGCGATCGGAGGAGGACCTTGTGACCAACCGGATCTGTTCTCCACGCGCGGTG 521

Qy 481 gttctctcaggacgcccattgtgttctgtagcagcgaggaagaaacagcctctgc 540
Db 522 GTGTCTTTAAGACGGGATGTGGTCTGTGATGACGCGCAGGCAACAGCCGTCGAGC 581
Qy 541 cacaacgtccctacacgcccgtgagccgacgcccgcgacacccgctgcccggcagsgta 600
Db 582 CACAACGTCGCTACGCGCTGGACGCGGACGCGCGGACGCGCGGCTGCGGCTT 641
Qy 601 ccgagatcagagtagtcaccaatatcatcaacgcccgggtcagtagtcggaatggccc-- 658
Db 642 CCAAGCTACGCGTGAATACATATTTATTCACGGCGCGGCTTCAATCGGAGATGGCCCG 701
Qy 659 ggaacgacgcccacgctgcacgcatcg---ctactacacgctgctactgcgcatgctcg 715
Db 702 GAACCGACCCCAACGCTGAATGGTGTGTACTTAAAGCCCCCTATGAGGATGTCTGG 761
Qy 716 gcaagccacgagggagcaacctgactgctacacccacagagaaacttgcg 763
Db 762 GGACGGGACACGAGGCAAACTTGTATGGTGTAAACCAAAAGGAACCTTG 809

RESULT 5 BF065067/c

LOCUS 829 bp mRNA EST 09-MAR-2001
DEFINITION HV_CEB0022N01f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEB0022N01f, mRNA sequence.

ACCESSION VERSION

BF065067
BF065067.1 GI:10841706

KEYWORDS SOURCE

Hordeum vulgare
barley.

ORGANISM REFERENCE

1 (bases 1 to 829)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.

TITLE JOURNAL

Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTACCCCTCACTAAAGG

High quality sequence stop: 589.

FEATURES source

1..829
/organism="Hordeum vulgare"
/cultivar="Cil16151 (M1a6)"
/db_xref="taxon:4513"
/clone="HV_CEB0022N01f"
library HVCDNA0005 (Erysiphe infected & control)
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
145 a 247 c 270 g 167 t

BASE COUNT ORIGIN

Query Match 73.9%; Score 569.6; DB 11; Length 829;
Best Local Similarity 90.9%; Pred. No. 5.4e-100;


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/db_xref="taxon:4513"
/clone="HV_CEB0006009f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVcDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 124 a 223 c 214 g 107 t 1 others
ORIGIN
Query Match 70.7%; Score 545.4; DB 10; Length 669;
Best Local Similarity 93.1%; Pred. No. 2.3e-95;
Matches 581; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 1 atggcgagtttgctgcctgcgcgtgtgcgccgcgcgcgtctctgcgcgtggcgcg 60
Db |||||||
QY 46 atggcgagccttgcctgcgcgtgtgcgccgcgcgcgtctctgcgcgtggcgcg 105
Db |||||||
QY 61 ggggtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
Db |||||||
QY 106 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 165
QY 121 ctgcccacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
Db |||||||
QY 166 CTGCGCAACCGCGACACCTCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCG 225
QY 181 atcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 240
Db |||||||
QY 226 ATCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 285
QY 241 cgcgcacctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
Db |||||||
QY 286 CCGGAGCTCGCGCGCTTCTTCGCGCAGACCTCCACGAGACACCGCGGAGGAG 345
QY 301 gctgcgaccagttccagtggtggtctgcttcaaggagagataagcaagccagtc 360
Db |||||||
QY 346 GCGCGCGACCACTTCCATGGGCGTACTGTTCAAGGAAGAGATAGCAAGGCCAG 405
QY 361 ccaccatactgagcggggaccatccaattgacagcgctccaactacatcttgc 420
Db |||||||
QY 406 CCACCTACTATGGACGGGAGCCATTCATTAATGACAGGCGGTCCAACTACGAT 465
QY 421 gggagagcgtcggaaggacactgtgagcaaccacgaactagtgtccacgacgcgtg 480
Db |||||||
QY 466 GGGAGAGCGATCGGAAGAGACCTTGTGAGCAACCCGCGATCTTGTGTTACGGAG 525
QY 481 gtgtccttcaggacggcctatgtgttcttgatgacggcgacggggaacaaagccgtg 540
Db |||||||
QY 526 GTGTCTTATACGGCGATGTGGGTCTGGATGACGGCGCAGGGCAACAGCGCTGAGC 585
QY 541 cac-aacgtcgccctacgcgtgtgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 599
Db |||||||
QY 586 CACAAACGTGGCCCTACACCGTGTGACGCCCGCGCGCGCGCGCGCGCGCGCG 645
QY 600 acccgatcacggagtgtacacaa 623
Db |||||||
QY 646 TCCAAGCTACGGTGTAAATCAACCA 669
Db |||||||
RESULT 9
BE214577
LOCUS BE214577 695 bp mRNA EST 09-MAR-2001
DEFINITION HV_CEB0003N19f Hordeum vulgare seedling green leaf EST library
HVCNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEB0003N19f, mRNA sequence.
ACCESSION BE214577
VERSION BE214577.2 GI:13264111
KEYWORDS EST.
SOURCE barley.

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ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 695)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, X., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
On Jul 3, 2000 this sequence version replaced gi:8902189.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACTCTCACTAAAGGG
High quality sequence stop: 638.
FEATURES
Location/Qualifiers
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/organism="Hordeum vulgare"
/cultivar="Cl16151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEB0003N19f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVcDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 133 a 227 c 218 g 116 t 1 others
ORIGIN
Query Match 69.9%; Score 538.6; DB 10; Length 695;
Best Local Similarity 91.9%; Pred. No. 4.7e-94;
Matches 568; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 33 cgcgcgcctcctgcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 92
Db |||||||
QY 76 CGCGCGGCTCTCTGCTCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 135
QY 93 catcacgcggtgcgtgtacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 152
Db |||||||
QY 136 CATCAGCAATCGGTGTACGCGAGCATGCTGCCCAACCGCGACACTCGATGCCCCGC 195
QY 153 cagaggtttctacgcgtacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 212
Db |||||||
QY 196 CAGGSGGTTCTACACGTACGACGCTTCATCGCGCGCGCGCGCGCGCGCGCGCGCT 255
QY 213 caccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 272
Db |||||||
QY 256 CACCACCGCGCAGCGCGCAGCGTCAAGCGCGAGCTCGCGCGCTTCTTCGCGCAGACT 315
QY 273 ccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 332
Db |||||||
QY 316 CCACGAGACTACCGGAGGACGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 375
QY 333 caaggagagataagcaagccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 392
Db |||||||
QY 376 CAAGGAGGAGATAACAAGCCACGCTCTCCACCTACTATGAGCGGNGACCATTCAA 435
QY 393 gacagggcggtccaactacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 452
Db |||||||
QY 436 GACAGGGCAGTCCAACTACGATCTCGCGGAGGCGGATCGGGAAGGAGGAGCTTGT 495
QY 453 ccagacacctagtgtccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 512

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Db 496 CCCGACCTGGTGTCCACAGACGGGTGGTGTCTTCCAGAACGCCATTGGTTCGTGAT 555
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Db 556 GACGCGCAGGAAACAGCGTGTGTCACAAAGTGTGCGCTACGCGTGTGACGCGAC 615
QY 573 GCGCGCAGACCGTGTGCGCGGAGGTGACCGGATGAGTGTGATGATGATGATGATGAT 632
Db 616 CGCTGCCGATACAGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 675
QY 633 GCGCGGCTGAGTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 650
Db 676 GCGCGGCTGAGTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 693

RESULT 10
LOCUS BE214283 725 bp mRNA EST 09-MAR-2001
DEFINITION HV_CEB0003A01f Hordeum vulgare seedling green leaf EST library
HV_CEB0003A01f (Erysiphe infected & control) Hordeum vulgare cDNA clone
ACCESSION BE214283
VERSION BE214283.1 GI:8901895
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 725)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAGGG
High quality sequence stop: 670.

FEATURES
source
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/organism="Hordeum vulgare"
/cultivar="C116151 (Mia6)"
/db_xref="taxon:4513"
/clone="HV_CEB0003A01f"
/clone_lib="Hordeum vulgare seedling green leaf EST
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/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 165 a 226 c 211 g 123 t
ORIGIN

Query Match 67.9%; Score 523.6; DB 10; Length 725;
Best Local Similarity 94.9%; Pred. No. 3.6e-91;
Matches 541; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 202 CCGGCTTCCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 261
Db 2 CCGGCTTCCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 61

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QY 262 ggcacagctccacagacacacgagagagagagagagagagagagagagagagagagag 321
Db 62 GCCAGACCTCCACAGACACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 121
QY 322 ggtactgtctcaaggaagagataagcaagggccacgctccccaccatactatggacggga 381
Db 122 GGTACTGTCTCAAGGAAGAGATAAGCAAGGCCACGCTCCACCTACTATGAGACGGGA 181
QY 382 cccatccaatgacagcgcggtccaaactagatcttccgggagagagatcggaagagac 441
Db 182 CCATCCAAATGACAGGGCGGTCCACTAGCATCTCCCGGGAGAGGATCGGGAAAGAC 241
QY 442 ctggtgagcaacccagacacctagtgtccacgagcggtgtgtctcttcagagagcgccatg 501
Db 242 CTTGTGAGCAACCGGATCTGTGTCTCCACGACGCGGTGTGTCTCTTACGACGGGATG 301
QY 502 tggttctggtatgacggcgaggggaaacacgcccgtctgcacaaacgtcgccctacgcgc 561
Db 302 TGGTTCTGTGATGACGGCGCAGGGCAACAAGCCGTTCGAGCCACAACGTCGCCCTACGCGC 361
QY 562 tggacgcgacgacgacgacacgctgctgcgaggggtacccgagatcgagtgatcacc 621
Db 362 TGGAGCGCGAGCGCGCGACACCGCTGCGCGTTCGCGGTTCAGGCTACGGTGTAAATCACC 421
QY 622 aatatcatcaacgcgcggtcgagtcgagtcggaatggcggaacgacgcaacgtcgaccgc 681
Db 422 CATATCATCAACGCGCGGCTCGAGTGGCGATGGCGGAGAACGACGCAACGTCATTCG 481
QY 682 atcgctactacacgctactcgcatctcgacgacgacgacgacgacgacgacgacgac 741
Db 482 ATGCGCTACTACACGCGCTACTCGCGCATCTCGGCGATCTCGGCGACGCGCGGGGCAACCTCGAC 541
QY 742 tgttacaccagaggaaacttcgctagctag 771
Db 542 TGCTACACCAACGGAACCTTCGCTAGCTAG 571

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RESULT 11
BF628657 713 bp mRNA EST 21-FEB-2001
LOCUS HVSMEB0006P01f Hordeum vulgare seedling shoot EST library
DEFINITION HVCDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
HVSMEB0006P01f, mRNA sequence.
ACCESSION BF628657
VERSION BF628657.2 GI:13090309
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 713)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Dec 19, 2000 this sequence version replaced gi:11892815.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAGGG
High quality sequence stop: 703.
Location/Qualifiers
1..713
/organism="Hordeum vulgare"
/cultivar="Morex"

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Tue May 7 10:52:34 2002

us-09-534-229c-6.rst

Page 12

Db 549 GACGGCCCAAGGCAACAG 567

Search completed: May 3, 2002, 16:23:53
Job time: 7193 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 15:34:10 ; Search time 3990.51 Seconds
(without alignments)
4018.348 Million cell updates/sec

Title: US-09-534-229c-7

Perfect score: 972

Sequence: 1 atctcacgctgagagcg.....ttgggtcgcgacagtga 972

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_yi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_om.*
20: em_or.*
21: em_ov.*
22: em_pat.*
23: em_ph.*
24: em_pl.*
25: em_ro.*
26: em_sts.*
27: em_sy.*
28: em_un.*
29: em_vi.*
30: em_htgo_hum.*
31: em_htgo_inv.*
32: em_htgo_rod.*
33: em_htg_hum.*
34: em_htg_inv.*
35: em_htg_rod.*
36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Match	Length	DB	ID	Description
1	590.8	60.8	1186	8	OSLMRNC	X56787 O.sativa L.
2	569.6	58.6	1779	8	BLYCHT3A	L34211 Hordeum vul
3	567.8	58.4	1291	8	RICCHIT3	L37289 Oryza sativ
4	561.2	57.7	1173	8	AF000965	AF000965 Poa prate
5	553.2	56.9	1080	8	AF000966	AF000966 Poa prate
6	543.4	55.9	1192	8	AF280437	AF280437 Secale ce
7	537.6	55.3	1051	8	OSD02286	U02286 Oryza sativ
8	537.4	55.3	1985	8	TACHIG	X76041 T.aestivum
9	536.4	55.2	1684	8	HV002287	U02287 Hordeum vul
10	536	55.1	1191	8	AB051578	AB051578 Secale ce
11	519.6	53.5	1252	8	AF000964	AF000964 Poa prate
12	518.4	53.3	2808	8	RICCHT3	D16223 Rice Cht-3
13	518.4	53.3	141534	2	AP003685	AP003685 Oryza sat
14	500.6	51.5	2739	8	RICCHT1	D16221 Rice Cht-1
15	496.6	51.1	1151	6	I84465	I84465 Sequence 2
16	490.6	50.5	1160	8	OSENDO	X56063 O.sativa mr
17	481.6	49.5	1237	8	OSCHIT	X54367 Oryza sativ
18	474.6	48.8	1159	8	OSCHITIA	Z29961 O.sativa (P
19	473.4	48.7	2048	8	OSDNARC24	X87109 O.sativa PC
20	469.4	48.3	998	8	BLYCHI	M62904 H.vulgare L
21	469.4	48.3	1002	6	A37990	A37990 Sequence 9
22	469.4	48.3	1002	6	AR037574	AR037574 Sequence
23	469.4	48.3	1002	6	I75200	I75200 Sequence 9
24	469.4	48.3	3169	8	BLYCHI26A	L34210 Hordeum vul
25	455	46.8	1018	8	AB051579	AB051579 Secale ce
26	450.8	46.4	2986	8	RICCHT2	D16222 Rice Cht-2
27	416.2	42.8	1280	8	AB018248	AB018248 Oryza sat
28	416.2	42.8	1300	8	AB012855	AB012855 Oryza sat
29	412.8	42.5	1120	8	PACHII	Z78202 Persea amer
30	407.4	41.9	1132	8	PHVCHM	M13968 P.vulgaris
31	405.4	41.7	892	8	AF307511	AF307511 Vigna ses
32	402.2	41.4	1146	8	VURNACHI1	X88800 V.unguicula
33	397.6	40.9	1100	8	OSCHITIB	Z29962 O.sativa (P
34	397.2	40.9	1128	8	MZECHITC	L00973 Zea mays ac
35	396.2	40.8	4704	8	S43926	S43926 CH5B-chitin
36	382.6	39.4	1058	8	AB015655	AB015655 Cucurbita
37	379.6	39.1	1070	8	AB048531	AB048531 Psophocar
38	375	38.6	879	6	E13289	E13289 cDNA encodi
39	375	38.6	998	6	E13290	E13290 cDNA encodi
40	371.6	38.2	1225	6	I23881	I23881 Sequence 1
41	371.6	38.2	1225	6	I92331	I92331 Sequence 1
42	369	38.0	1012	8	MZECHITINA	L16798 Zea mays cl
43	367.6	37.8	1007	8	ALCCHITIA	M94106 Allium sati
44	366.8	37.7	1670	8	PEACHIT2I	L37876 Pisum sativ
45	354.6	36.5	888	8	HBR238579	AJ238579 Hevea bra

ALIGNMENTS

RESULT	1					
OSLMRNC						
LOCUS	OSLMRNC	1186 bp	mrna	PLN	05-MAY-1995	
DEFINITION	O.sativa L. mrna for endochitinase.					
ACCESSION	X56787					
VERSION	X56787.1	GI:407471				
KEYWORDS	endochitinase.					
SOURCE	Oryza sativa.					
ORGANISM	Oryza sativa					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
AUTHORS	1 (bases 1 to 1186)					
TITLE	Nishizawa, Y., Kishimoto, N., Saito, A. and Hibi, T.					
JOURNAL	Sequence variation, differential expression and chromosomal					
MEDLINE	Location of rice chitinase genes					
REFERENCE	Mol. Gen. Genet. 241 (1-2), 1-10 (1993)					
AUTHORS	94049667					
	2 (bases 1 to 1186)					
	Nishizawa, Y.					


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/db_xref="GI:507961"
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WGYFRELGSPPDYSPSSQWPCVQDRQYGRGPIMLSNYNTGPRAGIAGVLLNN
PDVATATYFETALFWMTPOAKPSSHAVITGOWTPAAATAAAGRVPGYITNI
INGLEGCRGADSRVADRIGFYORYCNILGVYGNLDYINQRPFEVRELLIQRVTE"
BASE COUNT      410 a      515 c      475 g      379 t
ORIGIN

Query Match      58.6%; Score 569.6; DB 8; Length 1779;
Best Local Similarity 76.7%; Pred. No. 7.4e-69;
Matches 746; Conservative 0; Mismatches 199; Indels 27; Gaps 3;

QY 25 gcaagcgccgtcctgagcgtgtcctgtgctgagcg-----gcgcggtcacgcgcgcagc 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 GTGTGTGGCCATCGTGGCCATCGTCTGTGTGGCGGGCTCGGCATGGCCATGGTGTGCCG 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 79 gccagcagtcggctgcgaagcggcgcgcccaagtgcgcgactgcctgtgtgtgcagc 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 GCACAGCAGTGTGCTCCAGCGCGCGCGCGAGCTGCCGAACCTGCTCTGTGTGCAGC 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 cagttcggttctgoggcaccacacctccactactgcccgcgcgcgcgcgcgcgcagtc 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 CGCTTCGGTTACTCGCGCAGCACCCTCCGACTACTCGCGCGCGCGCTGCCAGAGCCAGTGC 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 199 actggtctcgg-----tgcgcgcgcgcgcggtggtgcctccatctg 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 AGCGCTCGGCGCCACACCCCTCCCGGCCCGAGCCCGCGCGGGGGGTGTGTCTCATCATC 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 tccagggacctcttgagcgttctctccatcgacgacgagcgtgcctgtgcccgc 300
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Db 940 TCCAGGGACCTTCTGAGCAGTTCCTCTCCACCG--CGACCGATGCCAAGATGCCGCC 996
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QY 301 ggggttcaacgtacgacgccttcttgccgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 997 GGGTTCACAGTACGACGCATTCCTGCGCGCGCGCGCACCTTCCTCCGCGCTTGGCCACC 1056
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 accggagacctggacacgcgaagcggagcgtggtggtggttcttggcgcagacacctcac 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1057 AGGGGAGCACCAGACCGGAGAGGAGTGGGGGCTTCTTCCGCGACACCTCCCAT 1116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 gagacacccgggttggccacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1117 GAGACACCGCGGTGTGGCCACCGCGCTGACGCGCCCTACTCTCGGGCTACTGCTAC 1176
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QY 481 aagcaggagcgggtctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 540
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Db 1177 AGCGGGAGCTGGGCTCGCGCCGACACTACTGCGCAGCCATCTCTCCAGTGGCGCGGTG 1236
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QY 541 ccgcgcaagcagctactatggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
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Db 1237 CAAGACAGCGAGTACTACGGCGCGGCCCCATCATGCTCTCATGGAATACAACTACGCG 1296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 ccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1297 CTGCGCGCGCGCGCATCGGGGTGAGCTGTGCAACAACCCGAGCTGGTGCCACGGAT 1356
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QY 661 ccgacagtggcgttcaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 720
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Db 1357 GCACCGGTCTCTCAGACGCGCATATGGTTCTTGATGACGCCGACGCCAACAGCGG 1416
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QY 721 tcgtgccatgactgacgggggtgtggtactccgagcgcgcgcgcgcgcgcgcgcgcgcgcgc 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1417 TCCTCTCAGCGCGTGTATCAGGGGCCAATGGAAGCGCGACGGCCGACAGACACCGCGGGGG 1476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 cgggtaccgcgggtatggtgtatcaacaacgtcatcaacgcgcgcgcgcgcgcgcgcgcgc 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1477 AGGGTGTCCCGGTACGGGGTATCATCAACAACATCATCAAGCGGGGCTCGAGTGCCTAGG 1536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 gggcagaacagcaaggtggcgatcgatcggtggttctcaaacgcgcgcgcgcgcgcgcgc 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1537 GGGGGGACACCGCGTGTGGCGACGGATGCGCTTCTTACCAGCGCTACTGCAACATCCTT 1596
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 ggcctggcctacgggaataacctgcactgcctacacccaattgtcttcaacgcttggttc 960
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1657 CTGATTCACGGA 1668
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT      3
LOCUS      RICCHITA      1291 bp      mRNA      PLN      30-OCT-1994
DEFINITION      Oryza sativa chitinase mRNA, complete cds.
ACCESSION      L37289
VERSION      L37289.1 GI:561872
KEYWORDS      chitinase.
SOURCE      Oryza sativa (strain IR36) seedling etiolated leaf cdna to mRNA.
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 1291)
AUTHORS      Yun,C.-H., Kim,J.-K. and Park,Y.-H.
TITLE      Isolation and Characterization of A Rice Chitinase cDNA
JOURNAL      Unpublished (1994)
FEATURES
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         /haplotype="2n=24"
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         /evidence=experimental
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         /protein_id="AAA51377.1"
         /db_xref="GI:561873"
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GWGSTSDYCGDGCQSCQSCGCGGGGGGGGGAVEAVVSKELPEOLLHNP
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GPTSWGCFKEEIAAASVCVSAEWPCAADKRYFGRIQSLSTNYNFGAGALGED
LLNPNLVASDPVVSFTALFWMTPOSPKPSCHDVITGOWTPSSGDIAAGRVPGYV
ITNININGLEGCGFPDDRVRANRIGFYORYCNLDYDQRPFNSGLAAVQ"
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         /function="chitinolytic activity, antifungal activity"
         /evidence=experimental
         /product="chitinase"
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Best Local Similarity 75.4%; Pred. No. 1.5e-68;
Matches 738; Conservative 0; Mismatches 202; Indels 39; Gaps 1;

QY 26 cgaagcgctcctgcgcgtgctcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 85
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Db 56 CGACAGCAGTGGCCCTCTCTCGTGGCGCGCGCCATGGTGGCGCAGTAGTCGCGCAGC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 86 agtcgcgctcgaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 AGTGTGGCTCGAGAGCGCGGTGGGGCGCTGTGCCCAACTGCTCTGTGTGACGCTCCTAGG 175
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JOURNAL Plant Physiol. 124 (3), 1251-1264 (2000)
PUBMED 11080301
REFERENCE 2 (bases 1 to 1192)
AUTHORS Yeh, S., Moffatt, B., Griffith, M., Xiong, F. and Hew, C.L.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2000) Biology, University of Waterloo, 200
University Ave West, Waterloo, ON N2L 3G1, Canada
LOCATION/Qualifiers
FEATURES
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/product="31.7 kDa class I endochitinase-antifreeze
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translation="MRGVVVVAMLAFAVSAHAEQCGSQAGGATCPNLCQSKFGPC
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FNQERGFSDYCSQWPCAPGKIFGRGPIQISINYNYPAGRAIGTDLNNDLV
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BASE COUNT 246 a 389 c 353 g 204 t
ORIGIN

Query Match 55.9%; Score 543.4; DB 8; Length 1192;
Best Local Similarity 75.0%; Ref. No. 3.2e-65;
Matches 704; Conservative 0; Mismatches 211; Indels 24; Gaps 1;

QY 34 gtctgagcggtgctgctgcggcgccggtgcacacggccgacgacgagcagtcgac 93
Db 61 GTGCTGTGCCATGCTGCGCGCGCTTCGCGCTGCTGTCACACCGCCGAGTGGCGG 120
QY 94 tcgacagcgggcgcccaagtgccgactgctgctgctgcgacgagtcggtgcttcgc 153
Db 121 TCGCAGCGCGCGCGCGCGCTGCCCACTGCTGCTGTCGACCAAGTTCGCTTCG 180
QY 154 ggcacacatccgactactgctggcccgctgcacagcagcagtcgctgctgctg 212
Db 181 GGTCTCCACTCCGAGTACTGCGCGCGAGCTGCCAGCGAGTCAACCGCTCGCGCG 240
QY 213 -----cgggcgggcggggtgctccatcgtgtccagggac 249
Db 241 ACACCACTACCGGTACCGACCCCGCGCGCGGTGTCCTTCATTCGCGAGTCG 300
QY 250 ctcttgagcggttctgtctcatcgcacacgacgagcgtgctgctgctgctgcttac 309
Db 301 CTCTTCGACGATGCTGTGTCACCGCAACGAGTGCCTGCTGCTGCGCAAGGGGTTC 360
QY 310 acgtacagcctcttggcgccgctgctgctgctgctgctgctgctgctgctgctg 369
Db 361 AACTAGCGGCTCTATCGCGCGCGCACTCGTCTGCGCTGCGCGTTCGCGACCGG 420
QY 370 ctggacacgagcgagcgaggtgctgctgctgctgctgctgctgctgctgctgctg 429
Db 421 ACCGAGGTGAGGAGCGGAGTGGCGGCTTCCTAGCTCAGACCTCCGACGAGCAC 480
QY 430 ggcgggtgacccacgacgacgacgacgacgacgacgacgacgacgacgacgacgag 489
Db 481 GCGGGGTGGCG 540
QY 490 cagggtcgccgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 549
Db 541 CG 600
QY 550 cagtactatgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 609

Db 601 AAGTACTTCGGCGCGCGCCCATCCAGATCTCATACACTACACTACGCGCGGG 660
QY 610 cgcgcaatcgggtgacactgctgaacaatcggacacgacgacgacgacgacgacgag 669
Db 661 CGGGCCATCGGACGAGCACTACTACACACCCAGACTCTGTGGCCACGACGCGCC 720
QY 670 gcggttaagacgcgagatgggttcctggatgacgacgacgacgacgacgacgacg 729
Db 721 TCATTTAAGACGCACTGTGTGATGACGCGCGACGACGACGACGACGACGACGAC 780
QY 730 gacgtgacacgaggtgctgacacgacgacgacgacgacgacgacgacgacgacg 789
Db 781 GACGTGATCAGCGCGCGTGGAGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 790 ggggtatggtcatcaccacgctcatcaacgctcgaacgacgacgacgacgacgac 849
Db 841 GGGTAGCGGTGATCACCACATCATCAACGGTGGCTCGAGTGGCGCGCGCGCG 900
QY 850 gacaaggtgagcgacgaggttcctacaagcgtattgacacgacgacgacgacgac 909
Db 901 GCTCGTGTGCGCGACGAAATCGGTTCTACAAGCGCTACTGTGACCTCTCGCG 960
QY 910 taggggaataaactgactgactgactgactgactgactgactgactgactgactg 948
Db 961 TAGGGCCACATCTGGACTGCTACACACGAGCGCGCTTC 999

RESULT 7
OSD02286
LOCUS Oryza sativa 1051 bp mRNA PLN 30-MAY-1994
DEFINITION Oryza sativa IR58 chitinase mRNA, complete cds.
ACCESSION U02286
VERSION U02286.1 GI:495302
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
TITLE 1 (bases 1 to 1051)
Anuratha, C.S., Mew, T. and Muthukrishnan, S.
Induction of chitinases and beta-glucanases in Rhizoctonia solani
infected rice plants: Isolation of an infection-related chitinase
cDNA clone
Unpublished
REFERENCE 2 (bases 1 to 1051)
AUTHORS Muthukrishnan, S.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1993) Muthukrishnan S., Kansas State University,
Biochemistry, Willard Hall, Manhattan, KS 66056, USA
FEATURES
source
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[illegible]

Db 884 GACGACCGCTGGCAAAACCGGATCGGCCTTCTTACCAGGCTACTTGGCGGCGGTTCGGCATC 943

Qy 907 ggctacggggaataacctcgactgctacaaccaatgttcgaacttggttgcgagcgttggtcgcg 964
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Db 944 GGACCGCGGCCAACCTCGACTGCTACAACGAGGCGCGTTCAAACGAGCGGTTCGCGG 1001
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RESULT 8

TACHIG TACHIG 1985 bp DNA PLN 02-AUG-1996
LOCUS T.aestivum (Chinese spring) chl gene for endochitinase.
DEFINITION X76041
ACCESSION T76041.1 GI:416028
VERSION X76041.1
KEYWORDS CHI gene; endochitinase.
SOURCE bread wheat.
ORGANISM triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1985)
AUTHORS Liao,Y.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH,
Worringer Weg, 52056 Aachen, FRG
REFERENCE 2 (bases 1 to 1985)
AUTHORS Liao,Y.C., Kreuzaler,F., Fischer,R., Reisner,H.J. and Tiburzy,R.
TITLE Characterization of a wheat class IB chitinase gene differentially
induced in isogenic lines by infection with Puccinia graminis
JOURNAL Plant Sci. 103, 177-187 (1994)
FEATURES Location/Qualifiers
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 /cultivar="Chinese spring"
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BASE COUNT 467 a 554 c 552 g 412 t
ORIGIN

Query Match 55.3%; Score 537.4; DB 8; Length 1985;
Best Local Similarity 74.5%; Pred. No. 1.7e-64;
Matches 704; Conservative 0; Mismatches 211; Indels 30; Gaps 1;


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DNGIICGHGQDSRDRIQGYFYRYCDILRVYGNNLDYCNQRPFA"
BASE COUNT      236 a   382 c   355 g   218 t
ORIGIN
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Best Local Similarity 74.2%; Pred. No. 3.3e-64;
Matches 708; Conservative 0; Mismatches 210; Indels 36; Gaps 1;

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    Ddb      64  GGTTTCGCGTGTGTTCCGCTGCCTGCCATGGCGGTGACCATGSCCTGCCGAGCAGTGC 123
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    QY      91  ggctcgcaagcggcgcgccgaagtgcgcgaactgcctgtgtcgcagccagttcggttc 150
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    QY     151  tcggcaccacctccgaactactcggcccccccgcgtccaaagccagtcgaactgactcggt 210
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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    QY     355  ggcacacacggagaccttgacaacgaggagcgaggtggcgctcttcttcggccaagacc 414
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    QY     415  tctcacgagacacacggcggtggccaacgcgcgcgaagccctctcatggggctac 474
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    QY     535  tcgcacacgcgaacagtagtatggccgcggcccataccagctcacccaccaactacaac 594
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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    QY     595  tacggaccgvcggcgcgccaatcggvggtggaactcgtgaacaatccggacctggtagcc 654
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:32:02 : Search time 309.71 Seconds
(without alignments)
2690.647 Million cell updates/sec

Title: us-09-534-229c-7
Perfect score: 972
Sequence: 1 atgtcacgctgagagcgcg.....ttgggctgcgagcacagtga 972

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543.4	55.9	954	AA24889	Rye chitinase-like
2	496.6	51.1	1151	AAQ31408	RCH10 chitinase ge
3	496.6	51.1	1151	AAQ81346	Rice chitinase RCH
4	496.6	51.1	3035	AAAF54983	Nucleotide sequenc
5	493.4	50.8	1163	AAAF5224	CDNA encoding a ma
6	469.4	48.3	1002	AAQ62518	Sequence encoding
7	416.2	42.8	1318	AAV49982	Floral organ-speci
8	396.2	40.8	4704	AAQ05264	Sequence encoding
9	375	38.6	879	AAQ79940	Chitinase coding s
10	375	38.6	998	AAQ79941	Full length chitin
11	370	38.1	1225	AAQ33325	American elm chiti

12	337.6	34.7	7397	20	AA235613	Banana ripening fr
13	316.8	32.6	1152	12	AAQ12898	Tobacco intracellu
14	316.8	32.6	1152	18	AAQ89952	Nicotiana sp. intr
15	316.8	32.6	1152	21	AAAF58910	CDNA sequence enco
16	304.2	31.3	756	20	AAQ24890	Rye chitinase-like
17	297	30.6	721	20	AAV69461	Banana fruit ripen
18	296.4	30.5	1118	21	AAAF6233	CDNA encoding a ma
19	289	29.7	755	20	AAV69463	Banana fruit ripen
20	285.4	29.4	802	20	AAV69462	Banana fruit ripen
21	278.6	28.7	1013	21	AAAF6231	CDNA encoding a ma
22	277	28.5	1077	21	AAAF6230	CDNA encoding a ma
23	265.2	27.3	583	21	AAAF6234	CDNA encoding a ma
24	238	24.5	769	20	AAV69464	Banana fruit ripen
25	226.2	23.3	768	20	AAV69466	Banana fruit ripen
26	205.2	21.1	991	21	AAQ41918	Arabidopsis thalia
27	196	20.2	1010	11	AAQ06185	PR-Q CDNA cloned i
28	196	20.2	1020	10	AAAF6211	PR-Q CDNA cloned i
29	196	20.2	1020	20	AAV62809	Tobacco PR-Q gene.
30	196	20.2	1020	20	AAV72995	Tobacco PR-Q gene
31	192.6	19.8	2636	19	AAV49983	Floral organ-speci
32	186	19.1	1619	21	AAAF6227	CDNA encoding a ma
33	185.6	19.1	1317	21	AAZ48613	Nettle lectin cDNA
34	185.6	19.1	1317	22	AAQ60211	Urtica dioica aggl
35	183	18.8	965	12	AAQ12897	Petunia extracellu
36	183	18.8	966	18	AAQ8951	Petunia hybrida ex
37	183	18.8	966	21	AAAF58909	CDNA sequence enco
38	176.8	18.2	730	20	AAV69465	Banana fruit ripen
39	175.2	18.0	968	11	AAQ06186	PR-P CDNA cloned i
40	175.2	18.0	968	20	AAV62813	Tobacco PR-P gene
41	175.2	18.0	968	20	AAV81601	PR-P protein encod
42	166.4	17.1	1116	21	AAAF6237	CDNA encoding a ma
43	163.2	16.8	1048	21	AAAF6232	CDNA encoding a ma
44	161.6	16.6	1153	13	AAQ21007	Sequence encoding
45	161.6	16.6	1153	15	AAQ68352	Endochitinase prec

ALIGNMENTS

RESULT 1
AA24889
ID AAX24889 standard; cDNA; 954 BP.
XX
AC AAX24889;
XX 21-JUN-1999 (first entry)
DT Rye chitinase-like protein CHT9 cDNA clone ch-9.
XX CHT9; chitinase-like protein; antifreeze protein; AFP;
KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW transgenic plant; preservation; cryopreservation; tumour; therapy;
KW ss.
XX Secale cereale.
OS
FH Key Location/Qualifiers
CDS 1..954
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FT /note= "separately claimed in Claim 2"
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WO9906565-A2.
11-FEB-1999.
31-JUL-1998; 98WO-CA00745.
31-JUL-1997; 97US-0903872.

XX	(ICEB-) ICE BIOTECH INC.
PX	Griffith M, Hew C, Moffatt B, Xiong F;
XX	WPI: 1999-153795/13
XX	P-FSDB; AAW98079, AAW98080.
DR	New nucleic acid encoding antifreeze polypeptides from plants -
PT	particularly with chitinase activity, used to impart frost, and
PT	pathogen, resistant to plants, for preservation of foods, cells etc.
PT	and for treating tumours
XX	
XX	Claim 2; Fig 21a; 118pp; English.
PX	The present sequence encodes winter rye (<i>Secale cereale</i> L. cv.
CC	Muskateer) CHT9 preprotein (see AAW98079). Mature CHT9 (see AAW98080)
CC	is a chitinase-like protein that has chitinase (antifungal) and
CC	antifreeze activities. CHT9 cDNA (ch-9) was obtained by isolating
CC	mRNA from rye plants grown at low temperatures in the absence of
CC	pathogens or other stresses, i.e. under conditions when only
CC	chitinases with antifreeze activity would be expressed, and then
CC	sorting the cold-induced chitinase cDNAs to determine which encoded
CC	proteins with ice-binding ability. CHT9 and CHT46 (see AAW98081-82)
CC	have been cloned and expressed in bacterial and yeast (<i>Pichia</i>)
CC	systems and in <i>Arabidopsis thaliana</i> . The chitinase-like antifreeze
CC	proteins can be used: to increase freeing tolerance of plants and
CC	microorganisms; to increase field survival of plants, animals and
CC	cryopreservation in biological materials or foods; to inhibit ice
CC	recrystallisation and hypothermic protection of cells, embryos,
CC	tissues etc. (particularly human platelets); and to kill tumour
CC	cells. They are also used to inhibit initiation and progression of
CC	diseases or spoilage caused by low temperature pathogens
CC	(particularly fungi) in plants, frozen foods and any cryopreserved
CC	biological material.
XX	
SQ	Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;
Query Match 55.9%; Score 543.4; DB 20; Length 954;	
Best Local Similarity 75.0%; Pred. No. 3e-86;	
Matches 704; Conservative 0; Mismatches 211; Indels 24; Gaps 1;	
QY	34 gtctggcgtgcttcttgccgcggcgccgagtcacgccggcgaggcacagtgcggc 93
Dd	
Db	13 gtagtgtgacctatgctggcgcggccttgccgtgctgtctgcacacgcagcagtcggc 72
QY	94 tcgaacgcggcgccgcacaaatgcgcgcactgctgtgctgcacgcagttcggttatgc 153
Dd	
Db	73 tgcgagccggcgggcgacgctgcccacaatgcctctgctgcagaagaatcggtttctgc 132
QY	154 ggaccacactccgactactcgccccccgctgcacagccagtcactggctcggtgg - 212
Dd	
Db	133 ggtccacctccagttactcgggcagcgctgcocagagcagtcgaaccgctcgcgcggc 192
QY	213 -----cggcgcggggggtggcctcatcggttcacaggagac 249
Dd	
Db	193 acaccagtaccggttacgaccccacacgcggcggtgctctcattctcgcagtcg 252
QY	250 ctcttcgagcgttcctgctccatcgacaacgacgacgctgcctggcccgggtttctac 309
Dd	
Db	253 ctcttcgaccagatgcctgtgcaccgcacgatgcgctgctggccaaggggtttctac 312
QY	310 acgtacagcgccttcttggccgcgcgcgcgcgttcctccgccttcggcacacoggagac 369
Dd	
Db	313 aaatacggccttcatcgccgcgcgaactcgttctcgggttcgcgacacgggttgc 372
QY	370 ctggacacgcggaagcgggagtggtggccctttctggccagacctctcagacacacc 429
Dd	
Db	373 accgacgtcaggaaagcgcgaggtggccgcgttctctagctcagacctccacagacacc 432
QY	430 gccgggtggcccacgcgcgcacgcgcgcctctctcatlyggggtactgctctcagcaggag 489

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RESULT	8	
AAQ05264		
ID	AAQ05264	standard; DNA; 4704 bp.
XX	XX	
XX	AAQ05264;	
XX	XX	
DT	23-NOV-1990	(first entry)
XX	XX	
DE	Sequence encoding bean chitinase gene fragment.	
XX	XX	
KW	Bean chitinase; phytopathogenic fungi; agrobacterium; ds.	
XX	XX	
CS	Phaseolus vulgaris var. SAXA.	
XX	XX	
EH	Key	Location/Qualifiers

RESULT 10
AAT79941
ID AAT79
XX
AC AAT79
XX
DT 13-OCT

Chromosome	Position (Mb)	Gene	RefSeq ID	Transcript Orientation	Strand	Transcript Length (nt)	5' UTR (nt)	Exon 1 (nt)	Intron 1 (nt)	Exon 2 (nt)	Intron 2 (nt)	Exon 3 (nt)	3' UTR (nt)	Stop Codon	
Db	736	ttcaaaacggcctta	ggtctctgga	gacccacag	tcaaccaag	ccctcgtg	ccatgac	795							
QY	733	gtatcac	ggggctgt	ggactc	gacggccag	ggatag	cgcagc	gccgag	gggtac	ccgg	792				
Db	796	gtatcac	gggaagat	ggagtc	ctccgg	cacgac	gaatg	cgccgg	cagagt	ggggc	855				
QY	793	tatggtgt	catcacc	aagctcat	caacggc	gggatcca	atg	cgcat	gggc	caga	aacgac	852			
Db	856	tacggc	ggtatc	accacatt	tcaac	ggtggg	atagat	gcgg	aaagtc	caggt	tcct	915			
QY	853	aaggtg	gcgatcg	ggttc	ctac	aagc	gcctat	gtg	aca	tttc	ggcat	gggtac	912		
Db	916	caggc	gggatc	ggattg	ctctaca	agaggt	actg	gat	cttc	tag	attgg	ctat	975		
QY	913	gggaata	acctc	gactg	ctac	acccaat	tgt	ggtt	ca	agctt	ggggc	ctc	960		
Db	976	gggaaca	aatctg	atgct	ata	acc	agag	gacctt	tgga	aatg	cactc	1023			

RESULT	12
AAAX25613	
ID	AAAX25613 standard; DNA; 7397 BP.
XX	
XX	AAAX25613;
XX	
DT	02-AUG-1999 (first entry)
XX	
DE	Banana ripening fruit Endo. DNA.
XX	
XX	Banana; fruit ripening; differential expression; fruit development;
KW	transgenic plant; ss.
OS	Musa acuminata.

PN	XX	WO9915668-A2.
XX		
PD	XX	01-APR-1999.
XX		
PF	XX	23-SEP-1998; 98WO-US03343.
XX		
PR	XX	25-SEP-1997; 97US-0060062.
XX		
PA	XX	(BOYC-) BOYCE THOMPSON INST PLANT RES.
XX		
PI	XX	Clendennen S, May G;
PI	XX	
XX		
DR	XX	WPI: 1999-244425/20.
DR	XX	P-PSDB; AAY05842, AAY05843, AAY05844.
XX		
XX		New isolated banana DNA molecules
PT		
XX		Claim 5; Fig 16A-J; 143pp; English.
XX		

This is the nucleotide sequence of a DNA molecule termed ENDO. The invention provides isolated DNA molecules which are differentially expressed during banana fruit development, and the protein products of these genes. The DNA is selected from a group comprising starch synthase, chitinase, endochitinase, beta-1,3-glucanase, thaumatin-like protein, ascorbate peroxidase, metallothionein, lectin and senescence-related protein. The regulatory elements of the genes can be used to produce chimeric genes for transformation of plants to provide controlled expression of heterologous DNA during fruit development, or in response to exogenous developmental signals, such as ethylene signals. The heterologous protein, e.g. a therapeutic protein, can be isolated from the fruit or consumed directly in the transformed fruit. The identity of the present sequence is not given. The entire DNA sequence has been decoded in all 3 reading frames to provide the amino acid sequences given in AAY05842-44.

SQ Sequence 7397 BP; 2109 A; 1549 C; 1592 G; 2012 T; 135 other;

[illegible]

CC The present sequence encodes an extracellular chitinase. The
CC specification describes transgenic plants which express a chitinase
CC gene and a glucanase gene. The expression of the chitinase and
CC beta-1,3-glucanase genes produces an antifungal effect. The transgenic
CC plants are useful for improving plant resistance to pathogenic fungi.
CC The recombinant polynucleotides and the process are useful for
CC producing fungal resistant plants.
XX

SQ Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;

Query Match 32.6%; Score 316.8; DB 21; Length 1152;
Best Local Similarity 61.5%; Pred. No. 6.1e-47;
Matches 545; Conservative 0; Mismatches 332; Indels 9; Gaps 2;

QY	71	cgccacgcccagcagctcggtccgaacgcccgcgcaagtcgcgcgactgcctgt	130
Db	58	ctgcctcggcagacaatatggttcgcaggcgggagcgctgtgcctcgggtctct	127
QY	131	gctgcagccagttcgggttctgcggcaccacctccgactactcggcccccgc---	187
Db	128	gctgcagcaaatgt	187
QY	188	agagccagtcacactg-----ctggggtggcggcggcggggtggcctccatcgt	241
Db	188	agagccagtcacactg-----ctggggtggcggcggcggggtggcctccatcgt	247
QY	242	ccagggaccctcttcgagcgttctcctgcctccatcgcaacgacgcagcgtgcctg	301
Db	248	caagttccatgtttgacacgatcttaagcatcgcaacgataatgatgcgaaggaa	307
QY	302	ggtctacacgtacgacgcctcttctggccgcgcgcgcgcgcgcgcgcgcgcgc	361
Db	308	gattctacagttacaatgcctttatcaatgctgtagtctcttctcgtggttgta	367
QY	362	ccggagaccttggacacgcgaagcggagatgcgccctctctcttcggcagaccc	421
Db	368	gtggtgataccactgcccgttaagagaaatcggcgttctctcgcacacacctcc	427
QY	422	agaccacggcgggtggccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	481
Db	428	aaactacagaggatgggcaacgaccagatggtccatagcgcgtgggttactgtgc	487
QY	482	agcaggagcaggc	541
Db	488	ttagagaacaatgagcccgcgactactgtacacacagtggtcagtgccctgtgct	547
QY	542	ccggcaagcagttactatggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	601
Db	548	ctggtcggaatatcttcggacgagcccccatacaatttcacacacacacacacac	607
QY	602	cggcggcgcgcgaatcggggtggacctgtgaacaatccggacctggtggccacgac	661
Db	608	cttgtggaagacgataggagtgacctcctaacaacctctgattagtgccacagac	667
QY	662	cgacagtggcgttcaagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	721
Db	668	cagtaactcattcaagtcagctcctctggtttggatgactcctcattccacaaacct	727
QY	722	cgtagcatgactgataccggggtgtgtgactccgcgcgcgcgcgcgcgcgcgcgc	781
Db	728	cttgccacgatgtcatcattggaagatggcaacctgctgctgcgcgcgcgcgcgc	787
QY	782	gggtaccgggtatgtgtcatcacaacgctcatcaacgcgcgcgcgcgcgcgcgcgc	841
Db	788	gtctcctcgtgattgtgtcatcagcaacatcatcaatggtggttggaatggtgctg	847
QY	842	ggcagacgacagagtggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	901
Db	848	gcactgactcaagggtccagagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	907
QY	902	gcacggctacgggaataacctgactgctacacacaaattgtcgtt	947

Db 908 gtgttagtctctgtgacaacattctgattgcggaacacagaggtcttt 953

Search completed: May 3, 2002, 16:32:50
Job time: 7004 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:26:33 ; Search time 142.45 seconds
(without alignments)
1545.361 Million cell updates/sec

Title: US-09-534-229c-7

Perfect score: 972
Sequence: 1 atgtccacgtgagagcgcg.....ttggcctgcgcacagtga 972

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA.*
1: /cgn2_6/prodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCITUS_COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	496.6	51.1	1151	1	US-07-704-288C-2
2	496.6	51.1	1151	1	US-08-093-372-1
3	496.6	51.1	1151	1	US-08-379-259-2
4	469.4	48.3	1002	1	US-08-457-797A-9
5	469.4	48.3	1002	1	US-08-812-025-9
6	469.4	48.3	1002	4	US-09-138-873A-9
7	371.6	38.2	1225	1	US-08-286-020-1
8	371.6	38.2	1225	1	US-08-603-919-1
9	318.4	32.8	943	2	US-08-475-427-15
10	318.4	32.8	943	2	US-07-842-165-15
11	316.8	32.6	1152	1	US-08-047-413-10
12	316.8	32.6	1152	3	US-08-229-050-10
13	316.8	32.6	1152	3	US-08-801-563-10
14	263.8	27.1	905	2	US-08-475-427-14
15	263.8	27.1	905	2	US-07-842-165-14
16	196	20.2	1020	1	US-08-181-271A-7
17	196	20.2	1020	1	US-08-449-315-7
18	196	20.2	1020	1	US-08-444-803-7
19	196	20.2	1020	1	US-08-449-043-7
20	196	20.2	1020	1	US-08-456-265A-7
21	196	20.2	1020	1	US-08-456-416-7
22	196	20.2	1020	1	US-08-455-244-7
23	196	20.2	1020	1	US-08-454-876-7
24	196	20.2	1020	2	US-08-457-364-7
25	196	20.2	1020	2	US-08-456-262-7
26	196	20.2	1020	2	US-08-456-240-7
27	196	20.2	1020	2	US-08-455-736-7

28	196	20.2	1020	2	US-08-971-217-7	Sequence 7, Appl
29	196	20.2	1020	4	US-09-350-600-7	Sequence 7, Appl
30	185.6	19.1	1317	3	US-07-791-931-1	Sequence 1, Appl
31	183	18.8	966	1	US-08-047-413-8	Sequence 8, Appl
32	183	18.8	966	3	US-08-229-050-8	Sequence 8, Appl
33	183	18.8	966	3	US-08-801-563-8	Sequence 8, Appl
34	175.2	18.0	968	1	US-08-181-271A-12	Sequence 12, Appl
35	175.2	18.0	968	1	US-08-449-315-12	Sequence 12, Appl
36	175.2	18.0	968	1	US-08-444-803-12	Sequence 12, Appl
37	175.2	18.0	968	1	US-08-449-043-12	Sequence 12, Appl
38	175.2	18.0	968	1	US-08-456-265A-12	Sequence 12, Appl
39	175.2	18.0	968	1	US-08-455-416-12	Sequence 12, Appl
40	175.2	18.0	968	1	US-08-455-244-12	Sequence 12, Appl
41	175.2	18.0	968	1	US-08-454-876-12	Sequence 12, Appl
42	175.2	18.0	968	2	US-08-457-364-12	Sequence 12, Appl
43	175.2	18.0	968	2	US-08-456-262-12	Sequence 12, Appl
44	175.2	18.0	968	2	US-08-456-240-12	Sequence 12, Appl
45	175.2	18.0	968	4	US-09-350-600-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 51.1%; Score 496.6; DB 1; Length 1151;
Best Local Similarity 72.4%; Pred. No. 1.9e-98;
Matches 684; Conservative 0; Mismatches 234; Indels 27; Gaps 2;

[illegible][illegible]

Db 837 GCGGGGCGGTCGCGGCTACGCGTTCATCACCAATCATCAACGCGGCTGGAGTG 896
QY 834 cggcagtgaggcagacacaaagtgccgagatcggtgttctacaaagcgtatttga 893
Db 897 CGGCATGGCGGAGGACGATCGCATCGCGGACCGATCGGCTTCTACAAAGGCTACTCGGA 956
QY 894 catttcggcagtcggtacgaggaataacccctcagctgctacaaacca 938
Db 957 CATCTCGGCTCAGCTACGCGGCGCACTTGGATGTGTACAGCCA 1001

RESULT 4
US-08-457-797A-9
Sequence 9, Application US/08457797A
Patent No. 5689045
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic pathogen-resistant organism
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,797A
FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..63
FEATURE:
NAME/KEY: CDS
LOCATION: 64..861
OTHER INFORMATION: /codon_start= 64
OTHER INFORMATION: /function= "chitinase"
OTHER INFORMATION: /product= "26 kD preprotein of chitinase G (ChiG)"
OTHER INFORMATION: /note= "antifungal activity, especially on
OTHER INFORMATION: Trichoderma reesei and Fusarium sporotrichoides as
OTHER INFORMATION: well as Rhizoctonia solani and Botrytis cinerea."
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 862..1002
OTHER INFORMATION: /partial
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NAME/KEY: polyA_signal
LOCATION: 905..910

OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
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FEATURE:
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OTHER INFORMATION: sequence"
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NAME/KEY: mat_peptide
LOCATION: 133..861
US-08-457-797A-9

Query Match 48.3%; Score 469.4; DB 1; Length 1002;
Best Local Similarity 76.6%; Pred. No. 3.5e-83;
Matches 575; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 198 cactggctgggtggcgggggggtggcctccatgtgtccaggagacctcttga 257
Db 108 CATGGCCATCGGCACGCGCGCGGCGGCTCTCCATGCTCTCGCGGCACAGTTGA 167

QY 258 ggggttcctgctccatcgaaacagcagcgtgcctggccggggtttctacacgtacga 317
Db 168 CCGCATGCTTCTCCACGCAACAGCAGCGCGCTTCCAGAGCCCAAGGGCTTACACCTACGA 227

QY 318 cgctttctggcgccgcccgcgttcccgcccttcgacacacgagacctggacac 377
Db 228 CGCCTTCGTGCGCGCGCGCGGCTTCCGCGGCTTCGGCACCACCGCGGCGGCGGAT 287

QY 378 gcggaagcgggaggtggcgcccttcttcggccagacctctcagagaccacggcggtg 437
Db 288 CCAGAAAGCGGAGGTGGCGCGCTTCTTAGCAGAGAGCTCCACAGAGACCGCGGCGTG 347

QY 438 gccacccgcccgcagcgcccttctcaggggctactcttcaagcaggagcagggtc 497
Db 348 GCGGACTGACCGGCGCGGCGGCTTCCGCTGGGGCTACTGCTTCAAGCAGAGAGAGTGGCGC 407

QY 498 gccgcgagctactgcgaccagagcgccgactggcgctgcgaccccggaagcagta 557
Db 408 CTCCTCCGACTACTGCAACCCCGGAGCGCACATGGCGGTGGCGCCCGGGAAGCGCTACTA 467

QY 558 tggcgcgcccatccatcagctcacccacataactacgagccggcgccgcaat 617
Db 468 CGGCGCGGCGGCAATCACTCTCCCAACTATGAGCTTCCGCGGCGGCGGCAAT 527

QY 618 csgggtgagacctcgaaacaatccggacctgtggccacgagcccgagacagtggttcaa 677
Db 528 CGGGGTGATCTGCTGGCGCAACCGGAGACTGTGTGGCGACGACCTGTGGGCTTTAA 587

QY 678 gacggcgatgtgttctgagacagcagtcacaaagccgtcgtgccatgacgtat 737
Db 588 GAGGCGCATCTGGTCTGGATGACGGCGGCGGCGGCGGCGGCGGCGGCTGTGTAT 647

Db 828 CAACCTCGATTGCTACAGCCAGAGACCCCTTC 858

Query Match 38.2%; Score 371.6; DB 1; Length 1225;
Best Local Similarity 64.5%; Pred. No. 3.3e-64;
Matches 573; Conservative 0; Mismatches 309; Indels 6;
Gaps

[illegible]

GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-842-165-14

Query Match 27.1%; Score 263.8; DB 2; Length 905;
Best Local Similarity 59.9%; Pred. No. 2.6e-43;
Matches 505; Conservative 0; Mismatches 317; Indels 21; Gaps 3;

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QY 71 cggccagcgccgagcagtcggtcgcaagccgagcgcccaagtcgacgactgcccgtgt 130
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 131 gctgcagcagttcgggttctgcggcaccacctccgactactcgcccccgc---tgcc 187
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 gttgcagcaaatcggtggtgcggtaacactaatgacattggttctgccaattgtc 181
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 188 agagcaagtgcactggtcggttgggc-----ggcgagcggttgccct 232
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 AAGTCAGTGTCCAGGTGGCGGCGCTCTGCTCTGTTACTGTTGGTGACCTCGGAA 241
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 233 ccattcgttcagggacctcttcgagcggttcttccttcctccatcgcaacgagcagcgtgcc 292
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 GCGTCATCTCAATTCATGTTTGATCAATGCTTAGCAATCGTAACGAAAATCTTGTC 301
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 293 tgg---cccggggttacacgtacgacgactcttggccgcgcgcgcgcgcgcgcgcgcgc 349
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 AAGGAAAGAAATAATTCTACAGTTACAAATGCTTAACTGCTGCTAGGTCITTTTCTCTG 361
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 ctttcgaccacgcgagcactggacacgcgggaagcgggaggttgccgactcttcggcc 409
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 362 GCTTTGTACAAGTGGTGATATCAATGCCGTAAAGGAAATGCTGCTTTCTTTGCC 421
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 agacctctcagagaccacgcgggtggtggccaccgcgcgcgcgcgcgcgcgcctctcatgg 469
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Search completed: May 3, 2002, 16:27:02
Job time: 7296 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:23:53 : Search time 3076.35 Seconds
(without alignments)
3395.224 Million cell updates/sec

US-09-534-229c-7

Title:

Perfect score:

Sequence: 1 atgtcaactgagagcgcg.....ttgggtcgccgacagtga 972

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estfun.*

2: em_esthum.*

3: em_estin.*

4: em_estom.*

5: em_estpl.*

6: em_estba.*

7: em_estro.*

8: em_estov.*

9: em_htc.*

10: gb_est1.*

11: gb_est2.*

12: gb_htc.*

13: gb_gss.*

14: em_gss_fun.*

15: em_gss_hum.*

16: em_gss_inv.*

17: em_gss_pln.*

18: em_gss_pro.*

19: em_gss_rod.*

20: em_gss_vrt.*

21: em_gss_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685.4	70.5	816	11 BF064981	HV_CEB002
2	566.4	58.3	652	10 AL499683	AL499683
3	533.6	54.9	693	10 AL500402	AL500402
4	520.2	53.5	616	10 BE405578	BE405578
5	471.6	48.5	508	10 BE430003	TAS006.A0
6	466.2	48.0	480	11 BG263207	WHE2339_C
7	455.6	46.9	805	11 BG365536	HVSMEL000
8	454.2	46.7	584	11 BE455567	HVSMEL000
9	429	44.1	935	11 BG365857	HVSMEL000
10	422.4	43.5	617	11 BF619746	HVSMEL000
11	414.2	42.6	729	10 BE602672	HVSMEL000
12	413.8	42.6	482	10 BE488961	WHE1077_C

13	403.8	41.5	623	11	BG368852	BG368852
14	403.6	41.5	937	11	BG365887	BG365887
15	403	41.5	498	10	BE425245	WHE313_A0
16	396.6	40.8	742	11	BG365634	BG365634
17	396	40.7	653	11	BG313150	WHE2054_D
18	394.4	40.6	682	11	BG416746	BG416746
19	394.4	40.6	806	11	BG414551	BG414551
20	392.4	40.4	402	10	BE498719	WHE0365_F
21	389.6	40.1	485	11	BF624146	BG368854
22	389.2	40.0	625	11	BG368854	BG368854
23	385.2	39.6	681	10	BE705117	Sc02_08b0
24	377.6	38.8	908	11	BG415203	HVSMEL000
25	372.4	38.3	731	10	BE602548	HVSMEL000
26	370.8	38.1	969	10	BE454366	HVSMEL000
27	363.4	37.4	711	11	BG366386	BG366386
28	356.4	36.7	711	10	BE455238	HVSMEL000
29	355.2	36.5	899	10	BE603335	HVSMEL000
30	354	36.4	489	10	BE411224	ISC003.D0
31	350.8	36.1	692	11	BG369588	BG369588
32	350.8	36.1	705	11	BG367460	BG367460
33	350.6	36.1	753	11	BG365326	BG365326
34	346.4	35.6	432	11	BF620099	HVSMEL000
35	346	35.6	717	10	BE454845	BE454845
36	345.4	35.5	613	10	BE425368	WHE313_F0
37	345.2	35.5	943	11	BG365157	BG365157
38	342	35.2	487	10	BE426069	WHE0327_A
39	340.4	35.0	711	11	BG367616	HVSMEL001
40	339.4	34.9	912	11	BG301220	HVSMEL001
41	338.2	34.8	710	11	BG366294	HVSMEL000
42	338	34.8	503	11	BG907369	BG907369
43	333.6	34.3	652	10	BE602137	TALr1159E
44	328.2	33.8	632	10	BE598085	BE598085
45	327.8	33.7	333	10	BE405888	P11_65_E1

ALIGNMENTS

RESULT 1

BF064981

LOCUS

DEFINITION

HV_CEB0022E17f Hordeum vulgare seedling green leaf EST library

HV_CEB0022E17f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Oct 17, 2000 this sequence version replaced gi:10841620.

Contact: Wing RA

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTACCTCCTACTAAGG

High quality sequence stop: 792.

Location/Qualifiers

1..816

/organism="Hordeum vulgare"

BF064981 816 bp mRNA EST 09-MAR-2001
HV_CEB0022E17f Hordeum vulgare seedling green leaf EST library
HV_CEB0022E17f, mRNA sequence.
BF064981
BF064981.2 GI:13266369
EST.
barley.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
Wing, R., Close, T.J., Klein, R., Wise, R., Begum, D., Frisch, D., Yu
Y., Anderson, H., Dale, J., Henry, D., Kern, S., Palmer, M., Rambo
T., Saski, C., Schwartz, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
On Oct 17, 2000 this sequence version replaced gi:10841620.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCCTACTAAGG
High quality sequence stop: 792.
Location/Qualifiers
1..816
/organism="Hordeum vulgare"

[illegible]

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quality sequence with phred score less than 20
Seq primer: Strategene SX primer.
FEATURES
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            /cultivar="Chinese Spring"
            /db_xref="taxon:4565"
            /clone="WHE1209_A02_A03"
            /clone_lib="Wheat etiolated seedling root cDNA library"
            /tissue_type="Root"
            /dev_stage="Five day old etiolated seedling"
            /lab_host="E. coli SOLR"
            /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                Site1: EcoRI; Site2: XhoI; Seeds were surface-sterilized
                , germinated and grown aseptically in the dark at room
                temperature on filter paper with water, nystatin and
                cefotaxime in covered crystallization dishes. Roots were
                harvested. The tissue, total RNA, and poly(A) RNA clones
                prepared, a cDNA library was made, and the cDNA clones
                were in vivo excised to give pBluescript phagemids in the
                TJ Clouse lab (Choi, Clouse, Fenton) at the University of
                California, Riverside. Plasmid DNA preparations and DNA
                sequencing were performed in the OD Anderson lab (all
                other authors)."
```

```

BASE COUNT      110 a      211 c      190 g      105 t
ORIGIN
Query Match      53.5%; Score 520.2; DB 10; Length 616;
Best Local Similarity 91.2%; Pred. No. 4e-86;
Matches 563; Conservative 0; Mismatches 53; Indels 1; Gaps 1;
Qy 120  ggaactgtgtgcagccagtcggttctgtggcggcagccacccctccgactactgcggccc 179
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 180  ccgctgcccagagccagtcgactgctggtggcgggcggggggtggcctccatcgt 239
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 240  gtcaggagacotcttcagagcgttctctgctccatcgacagcagcagcgtgcctggccg 299
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 300  caggtttacacgacacgacctctgtgcccgcgcgcgcgcgttcccgcccttcggcac 359
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 360  caccggagacctggacacgcggaagcggagtggtggcgcccttcttcggccagacccctca 419
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 420  cgagaccacggcggtggccacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 479
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 480  caagcagagcagcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 539
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 540  acccggcgaagcagtcactatggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 599
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 600  accgcgggccgcgcaatcgggtggacacgtgctgacacacccgaccccttcggtggccacgga 559
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 660  cccgacgtggcgttcaagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 719
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 720  gtcgtgcaatgacgtga 736
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```

FEATURES
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        1..508
            /organism="Triticum aestivum"
            /db_xref="taxon:4565"
            /clone="TAS006.A08"
            /clone_lib="ITEC TAS Wheat cDNA Library"
BASE COUNT      66 a      188 c      175 g      79 t
ORIGIN
Query Match      48.5%; Score 471.6; DB 10; Length 508;
Best Local Similarity 97.8%; Pred. No. 3.2e-77;
Matches 499; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
Qy 6  cagctgagagcgcggtgtgcgacgcccgtctcgtgcccgtcctctgcccgcgcgcgcgcgt 65
Db 1  CAGGCTGAGAGCGCGGTGTGCGACGGCGCTCTGTGGCCGCTCGTCTCTGTGGCGCGCGCGGT 60
Qy 66  cagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 125
Db 61  CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 126  cctgtgctgcgacgcagttcgggttctgcgcacacacctccgactactcgcgcgcgcgcgc 185
Db 121  CTTGTGCTGCAGCCAGTTCGGGTTCGTGCGGACACCACTCCGACTCTGCGGCGCGCGGTG 180
Qy 186  ccagagccagtcgactggtgcggtggcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 245
Db 181  CCAGAGCCAGTGCATGCTGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 246  ggaacctctcagcgcgttctcgtccatcgacacgcgcgcgcgcgcgcgcgcgcgcgcgcgc 305
Db 241  GGACCTCTTCGAGCGGTTCTCTCTCATCGCAACACGACGCGCTGCGCGCGCGCGGT 300
Qy 306  ctacacgtacgcgccttcttgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 365
Db 301  CTACACGTACGACGCTTCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
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Db 600 GTCATGCCATGACGTGA 616

RESULT 5

BE430003 508 bp mRNA EST 26-JUL-2000

LOCUS TAS006.A08R990616 ITEC TAS Wheat cDNA Library Triticum aestivum

DEFINITION cDNA clone TAS006.A08, mRNA sequence.

ACCESSION BE430003

VERSION BE430003.1 GI:9427846

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 508)

AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

TITLE International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae

JOURNAL Unpublished (2000)

COMMENT Contact: Selvaraj G

Plant Biotechnology Institute, National Research Council of Canada

110 Gymnasium Place, Saskatoon, SK S7N 0W9 Canada

Tel: 306 975 5577

Fax: 306 975 4839

Email: Gopalan.Selvaraj@nrc.ca

International Triticaceae EST Cooperative (ITEC)

http://wheat.pw.usda.gov/genome.

Location/Qualifiers

1..508

/organism="Triticum aestivum"

/db_xref="taxon:4565"

/clone="TAS006.A08"

/clone_lib="ITEC TAS Wheat cDNA Library"

66 a 188 c 175 g 79 t

Query Match 48.5%; Score 471.6; DB 10; Length 508;

Best Local Similarity 97.8%; Pred. No. 3.2e-77;

Matches 499; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Qy 6 cagctgagagcgcggtgtgcgacgcccgtctcgtgcccgtcctctgcccgcgcgcgcgcgt 65

Db 1 CAGGCTGAGAGCGCGGTGTGCGACGGCGCTCTGTGGCCGCTCGTCTCTGTGGCGCGCGGT 60

Qy 66 cagc 125

Db 61 CAGCG 120

Qy 126 cctgtgctgcgacgcagttcgggttctgcgcacacacctccgactactcgcgcgcgcgcgc 185

Db 121 CTTGTGCTGCAGCCAGTTCGGGTTCGTGCGGACACCACTCCGACTCTGCGGCGCGGTG 180

Qy 186 ccagagccagtcgactggtgcggtggcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 245

Db 181 CCAGAGCCAGTGCATGCTGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

Qy 246 ggaacctctcagcgcgttctcgtccatcgacacgcgcgcgcgcgcgcgcgcgcgcgcgcgc 305

Db 241 GGACCTCTTCGAGCGGTTCTCTCTCATCGCAACACGACGCGCTGCGCGCGCGGT 300

Qy 306 ctacacgtacgcgccttcttgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 365

Db 301 CTACACGTACGACGCTTCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

see <http://www.genome.clemson.edu/projects/barley/> To
order a clone see <http://www.genome.clemson.edu/orders>"

135 a	274 c	271 q	125 t
-------	-------	-------	-------

BASE COUNT

[illegible]

ORGANISM	Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum. 1 (bases 1 to 584)
REFERENCE	Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu T., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D. W., Main, D. and Wood, T.
TITLE	Development of a genetically and physically anchored EST resource for barley genomics
JOURNAL	Unpublished (2000)
COMMENT	On Jul 28, 2000 this sequence version replaced gi:9465371. Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7268 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: AATTAAACCTCACTAAAGGG High quality sequence stop: 567.

FEATURES	SOURCE
----------	--------

```

1: 360:
source
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEG0017N15f"
/clone_lib="Hordeum vulgare pre-anthesis spike EST library"
HVCNA0008 (white to yellow anther)"
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/note="vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
http://www.genome.clemson.edu/orders"

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BASE COUNT
ORIGIN

[illegible]

RESULT	8	
BE455567		
LOCUS	BE455567	584 bp mRNA
DEFINITION	HVSMeg0017N15f Hordeum vulgare pre-anthesis spike EST library	29-MAY-2001
	HVSCNA0008 (white to yellow anther) Hordeum vulgare cDNA clone	
	HVSMeg0017N15f, mRNA sequence.	
ACCESSION	BE455567	
VERSION	BE455567.2	GI:13154876
KEYWORDS	EST.	
SOURCE	barley.	


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|||||
Db 429 GAGACACCGCGGCTGCTACCGGCTCGACAGCCCTTCCTCGTGGAGGCTGCTTC 488
Qy 481 aagcaggacgggctgccccgagctactcga-ccagagcgcgactgccctggc 539
|||||
Db 489 AAGCAGGAGCGAGCTCGACGCGGAGCTACTGAGACCCAAAGCCCGACTGCGCCGCGC 548
Qy 540 accggcagcagtactatggcggcgcccccacc 574
|||||
Db 549 GCCACGACAGCTGCTTGGCCGCGGCCCATCC 583

RESULT 9
LOCUS BG365857 935 bp mRNA EST 08-MAR-2001
DEFINITION HVSMF0004109f Hordeum vulgare 20 DAP spike EST library HVcDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMF0004109f, mRNA sequence.
ACCESSION BG365857
VERSION BG365857.1 GI:13254956
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 935)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTCAATAAGG
High quality sequence stop: 626.
Location/Qualifiers
FEATURES
source
1..935
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMF0004109f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HVcDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/notes="Vector; lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 151 a 338 c 290 g 156 t
ORIGIN

Query Match 44.1%; Score 429; DB 11; Length 935;
Best Local Similarity 72.0%; Pred. No. 2.3e-69;
Matches 643; Conservative 0; Mismatches 215; Indels 35; Gaps 5;

Qy 27 gacggcgctctggcgcgtcgcttcctggcgccggcggtcagcgccgacggcgagca 86
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Db 39 GAGAGCGTTCGTGTGTCGCCGCTGGTGTGCATGCGGCCAGCAAGCGCTGCGCGAGCA 98
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Qy 87 gtggcgctcgcaagcgcgccgagtcgcaagtgcctgtgctgcaagccagttcg 146
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Db 99 GTGCGGCTCGCAGGCGCGGGGACCTGCCCAACTGCTCTGCTCAGCGGCTCGG 158
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Qy 147 gttctgggaaccacctcgactactgcgcccccgctgcccagagccagtgcaactggctg 206

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Db 159 CTGGTGGGCTCCACCTCGGACTACTTGGCGGACGGATGCCAGCCATGCTCGGCTG 218
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Qy 237 cgtgtccagggacctcttcagcgggttcctgtctcctcgaacgacgagcgtgcctggc 296
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Qy 297 ccgcggtttcacgtagcagcctcttggccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 356
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Qy 357 caccacccgagagcactgacacgcggagcggaggtggcgcccttcttggccagacctc 416
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Qy 417 tcacgagaccccgcggtgtggccacccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 476
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Qy 477 cttcaacgaggaacagggctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 536
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Qy 537 cgaccgcggcaagcagctactatggcgcgccccctccagctccaccacaaactacaacta 596
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Qy 597 cgaccgcggcgcgcaactcgggtggacctgctgaacaaatccgacctgtgccac 656
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Qy 657 ggaccgacagtggttcaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 714
Db 699 CGACCCGACCGTGTCTGTTTAAACTGCGATGTGTTTGGATGNAACGGCCAGCGCCAA 758
Qy 715 aagcgcgtcgtgcatgacgtgataccgggggtgt-ggactccgacggccagggatagcg 773
Db 759 AGCGTCTGAGGCTCTCTCTGATCACCAGCAATGGGACCCCTTAAGAACAGGACCGCGG 818
Qy 774 agccggacgggt-accgggtatggtgtcattcaccacgctcacaacggcggtatccaat 832
Db 819 AGTGGCGCGGTGCGCGGGTTTGTCTATTACCATTTGTAACGCGCTGGATCGAAT 878
Qy 833 -gcggcatggggcagaacgacaagtgcgcgatcgatcggtgtctacaagcg 884
Db 879 GCGGCGCTTGGCCAGACATCCCAATCCCGACGCTATCGGGTTTAAACGCG 931

RESULT 10
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LOCUS HVSMF0009B09f Hordeum vulgare seedling shoot EST library
DEFINITION HVcDNA0003 (Btolated and unstressed) Hordeum vulgare cDNA clone
HVSMF0009B09f, mRNA sequence.
ACCESSION BF619746
VERSION BF619746.2 GI:13107773
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 617)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
Development of a genetically and physically anchored EST resource
for barley genomics

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Qy 579 caccacaa 587
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Db 489 CACTCACAA 497

Search completed: May 3, 2002, 16:24:10
Job time: 7210 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 15:36:53 ; Search time 3990.51 Seconds
(without alignments)
3968.739 Million cell updates/sec

Title: US-09-534-229c-8

Perfect score: 960

Sequence: 1 atgagaggagtgtgtgtgtgt.....accaaagccgttgcagatag 960

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

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3: gb_in:*
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5: gb_ov:*
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32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB	ID	Description
1	875	91.1	1985	8	TACHIG	X76041 T.aestivum
2	852.8	88.8	1192	8	AF280437	AF280437 Secale ce
3	800.4	83.4	1173	8	AF000965	AF000965 Poa prate
4	796.6	83.0	1080	8	AF000966	AF000966 Poa prate
5	777.4	81.0	1252	8	AF000964	AF000964 Poa prate
6	634	66.0	2808	8	RICCHT3	D16223 Rice Cht-3
7	634	66.0	141534	2	AP003685	AP003685 Oryza sat
8	630.8	65.7	1684	8	HVU02287	U02287 Hordeum vul
9	629.6	65.6	1191	8	AB051578	AB051578 Secale ce
10	621	64.7	2739	8	RICCHT1	D16221 Rice Cht-1
11	614.6	64.0	1151	6	I84465	I84465 Sequence 2
12	612	63.8	1160	8	OSENDO	X56063 O.sativa mR
13	598.4	62.3	1186	8	OSLMNAC	X56787 O.sativa L.
14	589.2	61.4	1237	8	OSCHIT	X54367 Oryza sativ
15	577.6	60.2	2048	8	OSDNARC24	X87109 O.sativa RC
16	574.8	59.9	1159	8	OSCHIT1A	Z29961 O.sativa (P
17	573.6	59.8	1291	8	RICCHITA	L37289 Oryza sativ
18	557.4	58.1	1779	8	BLYCHI33A	L34211 Hordeum vul
19	530.8	55.3	1051	8	OSU0286	U02286 Oryza sativ
20	528	55.0	1018	8	AB051579	AB051579 Secale ce
21	513.6	53.5	998	8	BLYCHI	M62904 H.vulgare L
22	513.6	53.5	1002	6	A37990	A37990 Sequence 9
23	513.6	53.5	1002	6	AR037574	AR037574 Sequence
24	513.6	53.5	1002	6	I75200	I75200 Sequence 9
25	513.6	53.5	3169	8	BLYCHI26A	L34210 Hordeum vul
26	491.8	51.2	1128	8	MZECHITC	L00973 Zea mays ac
27	470.8	49.0	1100	8	OSCHITIB	Z29962 O.sativa (P
28	458.4	47.8	2986	8	RICCHT2	D16222 Rice Cht-2
29	441.4	46.0	1300	8	AB012855	AB012855 Oryza sat
30	439.8	45.8	1280	8	AB018248	AB018248 Oryza sat
31	428.4	44.6	1120	8	PACHI1	Z78202 Persea amer
32	408.8	42.6	1012	8	MZECHITINA	L16798 Zea mays cl
33	400	41.7	1085	8	ALCCHITIN	M94105 Allium sati
34	392	40.8	556	8	HVENDCHT	X15349 Barley (H.v
35	387.2	40.3	1132	8	PHVCHM	X13968 P.vulgaris
36	377.2	39.3	1058	8	AB015655	AB015655 Cucurbita
37	376	39.2	4704	8	S43926	S43926 CH5B-chitin
38	375.4	39.1	1132	8	NTECHITR	X16939 Nicotiana t
39	371.8	38.7	1070	8	AB048531	AB048531 Psophocar
40	371.6	38.7	1007	8	ALCCHINTIA	M94106 Allium sati
41	369.2	38.5	879	6	E13289	E13289 cDNA encodi
42	369.2	38.5	998	6	E13290	E13290 cDNA encodi
43	365.4	38.1	1670	8	PEACH12I	L37876 Pisum sativ
44	362.6	37.8	1156	8	S44869	S44869 basic chiti
45	359.8	37.5	892	8	AF307511	AF307511 Vigna ses

ALIGNMENTS

RESULT 1

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LOCUS T.aestivum (Chinese spring) chi gene for endochitinase.
DEFINITION X76041
ACCESSION X76041.1 GI:416028
VERSION X76041.1
KEYWORDS CHI gene; endochitinase.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1985)
AUTHORS Liao,Y.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH,
Worringer Weg, 52056 Aachen, FRG
REFERENCE 2 (bases 1 to 1985)
AUTHORS Liao,Y.C., Kreuzaler,F., Fischer,R., Reisener,H.J. and Tiburzy,R.
TITLE Characterizatiotn of a wheat class Ib chitinase gene differentially


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Db      766  AACCTTCGACGACGACGTGATACACGGCGCGGTGGAGCCCTCGGGCGCCGACGACGA 825
QY      781  gcgggaggggtgcctgggttacggtgtgatcaccacaatcatcaacggtgggtcgatgctc 840
Db      826  GCGGTAGGGTGCCTGGGTACGGCGTGTATCACCACCAATCATCAACGGTGGGCTCGAGTGC 885
QY      841  ggcgcggggcagacagccgctgtgcgcgacggatcgggttctacaagcgtactgcgac 900
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QY      901  ctcttggcgtcagctacggtgacaaactggactgtacaaacaaagccgttgcgcatg 960
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RESULT 3
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ACCESSION      AF000965
VERSION      AF000965.1 GI:6164586
KEYWORDS      Kentucky bluegrass.
SOURCE      Poa pratensis
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poaceae; Poa.
1 (bases 1 to 1173)
Du, M. and Ha, S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, CA
94706, USA

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Matches 865; Conservative 0; Mismatches 86; Indels 3; Gaps 1

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Qy      61  gagcaatcgcgctgcagggcgggggagcgtgcccaactgcctctgtgcgagcaag 120
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Qy      241  attatctgcagtcgctttgcaccagatgctgtgcaccgcaacagacggcgatgcctg 300
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AB051578
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ACCESSION AB051578
VERSION AB051578.1 GI:11344586
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SOURCE Secale cereale cDNA to mRNA.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Secale.
REFERENCE
1 (sites)

AUTHORS Ohnuma,T., Yamagami,T. and Ishiguro,M.
TITLE Cloning and Sequencing of the Rye Seed Chitinase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1191)
AUTHORS Ohnuma,T., Yamagami,T. and Ishiguro,M.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-2000) to the DDBJ/EMBL/GenBank databases. Takeshi Yamagami, Kyushu University, Protein Chemistry and Engineering, Faculty of Agriculture; Hakozaki, 6-10-1, Fukuoka, Higashi-ku, Fukuoka 812-8581, Japan (E-mail:yamagami@uclink.berkeley.edu, Tel:81-92-642-4218, Fax:81-92-642-3051)
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QY 121 ttgggtttctgcggcaccacctcgcactactcgtgcggcaccggtgcagagccagtgcaat 180
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QY	61 gagcaatgcggtctgcagcgcggcggaactgccccaaactgcctctgcagcaag	120
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QY	121 ttcggttttcggcacaccactccgactactgcggcaccggctgcagagcagtgcaat	180
Db	1438 TAGCGTGTGGGATCCACTTCGGCCTACTTGGCGCTCCGGCTGCCAGACCAGTGCTCC	1497
QY	181 g---gctgcagcggcggaaccccoggtaccggtaaccgaaccccttcggcgggcggtctcc	237
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QY	238 tcatttatctcgagtcgctcttcgacagatgctgctgcaccgcaaacgcgcggcgctgc	297
Db	1558 TCATATCGTGTGCGCTCGCTCTGACCATGCTTCTCCACCGCACGACGCGCGCTGC	1617
QY	298 ctggccaagggtttctacaactacgpgccttcgtccgcgcgcacaaactggttctcgggc	357
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QY	358 ttgcgaccacagtagcacgcagctcaagaagcgcagatggcgcgcttcctcgctcag	417
Db	1678 TTGCCAACACCGCGGACGCGCCGACCCGGAAGCGCGAGGTGCGCGGCTTCTTCTGGCGCAG	1737
QY	418 acttccacacagacgcgcgggttgccgacggcgcccgacggccctactcctggggc	477
Db	1738 ACGTTCGACGAGACCAGGCGGGTGGGCGACGCGCCCGATGCCCCCTACTCTGFGGGC	1797
QY	478 tactgtctcaaccaggagcgcggcgcaacc-----tcgactactgcacgcagactcg	531
Db	1798 TACTGCTCAAAGAGGAGAGAACAGCGCAAGCTTGGGTCCGACTACTGTGTCCAGAGCTCG	1857
QY	532 cagtgacctgtgcgcggcaagaagtacttcggcgcgagggcccatccagatctcac	591
Db	1858 CAGTGGCCGTCGCGCCGCGGCAAGTACTACGGCGGGGACCCATCCAGATCTCTCAT	1917
QY	592 aactacaactacggcgcgggcgagggcattcgcgcacccgacctgctcaacacccggac	651

[illegible]

Db 1476 GACGTGCGACAGACCATGGCGGGTGGCGGACGCGGCCGCGATGGCCCTACTCTGTGGG 1535
QY 477 ctactgtcttaaccaggagcgcgccacc-----tcgactactgaagccgagctc 530
Db 1536 CTACTGCTTCAAGAGGAACACGCGACGTGGTCCGACTACTGTGCCAGAGCTC 1595
QY 531 gcagtggccatgtgcgcgggcaagaagtacttggcgcgcccatccagatctcaca 590
Db 1596 GCAGTGGCGGTGCGCGCGGCAAGAAGTACTACGCGCGGGGACCCATCCAGATCTCTTA 1655
QY 591 caactacaactacggcgccggcgaggccatcggaacgcactgctcaacaacccgga 650
Db 1656 CAACTACAACTACGGCCCCGGGGGAGGCCATCGGCTCCAACTGCTGAGCAACCCGGA 1715
QY 651 ccttggcggtcgagacgcgcgtgtcgtttaagacggcggttgggttcttgatgacgcc 710
Db 1716 CC---TGGCGTGGAGCGCCACCGTCTCTTCAGACGGCGTCTTGTTCTGGATGACGCC 1772
QY 711 gcaatcaacccaagccttcgagccacacgtgatcacggcgccgtggagccctcggggc 770
Db 1773 GCAGTGGCGCAAGCCGTCGTGCCACGCGGTGATGACAGGCGAGTGGACGCCCAACGCCAA 1832
QY 771 cagaccagcgcgaggaggtgcttggtacgtgtgatcaccacaacatcaacgtgg 830
Db 1833 CGACCAAGCGCGGGGCGCGTGCCTGGGCTACGGCGTGGTGACCAACATCATCAACGGCGG 1892
QY 831 gctcgagtgcggcgcgaggacgcgcgtgtcgccgacccggtcggttctacaagcg 890
Db 1893 CGTGGAGTGGCGCCACGGCGCGNACAGAGTCCGCGACCGGATTGGGTTCACAGCG 1952
QY 891 ctactcgacctccttggcgctcagctacggtgacaacctggaactgtacaacccaaagcc 950
Db 1953 CTACTGGACATGTTGGGCGTCACTACGGCGCCAACTTGGACTGCTACAAACAGAGGCC 2012
QY 951 gtic 954
Db 2013 TTTC 2016

Search completed: May 3, 2002, 15:39:33
Job time: 4662 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:32:50 ; Search time 309.71 Seconds
(without alignments)
2657.429 Million cell updates/sec

Title: US-09-534-229c-8

Perfect score: 960

Sequence: 1 atgagagggtgtgtgtgt.....accaaaggcgttcgcatag 960

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_1101.*

1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT.*
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12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	854.6	89.0	954	AA24889	Rye chitinase-like
2	614.6	64.0	1151	AAQ31408	RCH10 chitinase ge
3	614.6	64.0	1151	AAQ81346	Rice chitinase RCH
4	611.4	63.7	3035	AAQ54983	Nucleotide sequenc
5	600.2	62.5	21	AAQ96224	cDNA encoding a ma
6	513.6	53.5	1002	AAQ62518	Sequence encoding
7	441.4	46.0	1318	AAV49982	Floral organ-speci
8	379.2	39.5	7397	AAQ25613	Banana ripening fr
9	374.4	39.0	4704	AAQ05264	Sequence encoding
10	369.2	38.5	879	AAQ79940	Chitinase coding s
11	369.2	38.5	998	AAQ79941	Full length chitin

12	358	37.3	1225	17	AAT33325	American elm chiti
13	347.6	36.2	1152	12	AAQ12898	Tobacco intracellu
14	347.6	36.2	1152	18	AAQ89952	Nicotiana sp. intr
15	347.6	36.2	1152	21	AAQ58910	cDNA sequence enco
16	323	33.6	721	20	AAV59461	Banana fruit ripen
17	320.8	33.4	755	20	AAV59463	Banana fruit ripen
18	308.2	32.1	1118	21	AAQ96233	cDNA encoding a ma
19	307	32.0	802	20	AAV59462	Banana fruit ripen
20	306	31.9	1013	21	AAQ96231	cDNA encoding a ma
21	301.4	31.4	756	20	AAQ24890	Rye chitinase-like
22	274.6	28.6	583	21	AAQ96234	cDNA encoding a ma
23	260	27.1	768	20	AAV59466	Banana fruit ripen
24	259.2	27.0	769	20	AAV59464	Banana fruit ripen
25	246	25.6	1077	21	AAQ96230	cDNA encoding a ma
26	222.2	23.1	991	21	AAC41918	Arabidopsis thalia
27	203.4	21.2	2636	19	AAV49983	Floral organ-speci
28	194.4	20.2	730	20	AAV59465	Banana fruit ripen
29	186.6	19.4	1317	21	AAC48613	Nettle lectin cDNA
30	186.6	19.4	1317	22	AAC60211	Urtica dioica aggl
31	178	18.5	1010	11	AAQ06185	PR-Q cDNA cloned i
32	178	18.5	1020	10	AAQ90845	Tobacco PR-Q gene
33	178	18.5	1020	20	AAV62809	Tobacco PR-Q gene
34	178	18.5	1020	20	AAV72995	PR-Q protein encod
35	177.2	18.5	968	11	AAQ06186	PR-P cDNA cloned i
36	177.2	18.5	968	20	AAV62813	Tobacco PR-P gene
37	177.2	18.5	968	20	AAV81601	PR-P protein encod
38	173.8	18.1	1153	13	AAQ21007	Sequence encoding
39	173.8	18.1	1153	15	AAQ68352	Endochitinase prec
40	173.8	18.1	1160	13	AAQ21193	Sequence of chimera
41	173.8	18.1	1863	13	AAQ21191	Sequence of chimera
42	173.8	18.1	1863	15	AAQ74261	Tomato-tobacco end
43	169.2	17.6	965	12	AAQ12897	Petunia extracellu
44	169.2	17.6	966	18	AAQ89951	Petunia hybrida ex
45	169.2	17.6	966	21	AAQ58909	cDNA sequence enco

ALIGNMENTS

RESULT 1

AA24889
ID AAX24889 standard; cDNA; 954 BP.
AC AAX24889;
XX
XX
DT 21-JUN-1999 (first entry)
XX
XX Rye chitinase-like protein CHT9 cDNA clone ch-9.

XX CHT9; chitinase-like protein; antifreeze protein; AFP;
KW winter rye; antifungal; fungicide; cold tolerance; frost tolerance;
KW transgenic plant; preservation; cryopreservation; tumour; therapy;
KW ss.

XX Secale cereale.

XX Key Location/Qualifiers

FT CDS 1..954

FT /*tag= a

FT /note= "separately claimed in Claim 2"

FT sig_peptide 1..60

FT /*tag= a

FT mat_peptide 61..954

FT /note= "separately claimed in Claim 2"

XX WO9906565-A2.

PD 11-FEB-1999.

XX 31-JUL-1998; 98WO-CA00745.

XX 31-JUL-1997; 97US-0903872.


```
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX Lamb CJ, Zhu Q;
XX WPI; 1992-415785/50.
XX P-PSDB; AAR29019.
XX DNA fragment contg. chitinase gene and its regulatory region - is
XX responsive to mature plant stress and has low level expression in
XX leaves, moderate level expression in stem and high level
XX expression in roots
XX Disclousure; Page 33-34; 45pp; English.
XX The sequence given represents the rice chitinase gene. The promoter
XX region of this gene (see AQ031407) is responsive to physical and/or
XX biological stress. The pattern of expression of this gene in mature
XX plants is characteristic. There is a low level of expression in
XX leaves, a moderate level in plant stems and the highest level in roots
XX and the male and female parts of the plant. The chitinase promoter
XX sequence may be linked to a reporter gene for expression in mono- or
XX dicotyledon plants. Expression of this reporter gene may be used to
XX study patterns of development and controlled expression of plant
XX defence genes and selectable genes.
XX Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;

Query Match          64.0%; Score 614.6; DB 13; Length 1151;
Best Local Similarity 80.3%; Pred. No. 4.6e-101;
Matches 773; Conservative 0; Mismatches 179; Indels 11; Gaps 4;

QY 1 atgagagagttgtgtgtgcccactgtgcccggccct---tcgccgtgtctgcgcac 57
DB ||||| ||| | ||||| ||||| ||||| ||| ||| ||| ||| |||
QY 58 ggcgagcaatgcggtcgcagccgcggcgagcgtgcccaactgctctgtctgcagc 117
DB ||||| ||| ||| ||||| ||||| ||| ||||| ||||| ||| ||||| |||
DB 115 ggcgagcagtcgagccagccgagccggcggtgtgcccaactgctctgtctgcagc 174
QY 118 aagttcgtttctgcgcacacactccgactactgcgcagcgcgtgcagagccaagtgc 177
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 175 cagttcgggtgtgtgtgtccactccgactactgcgcgcggatgccagagccaagtgc 234
QY 178 -aattgctcagcgccgcaccccggtaccgtaccacccctccggcgccggtctc 236
DB ||||| ||| ||||| ||||| ||||| ||| | ||| ||||| |||
DB 235 tcgcggctcggcgccgcccgcg---acgctcggcgccggtggtgcagcggtctgc 290
QY 237 ctccattatctgcagtgctcttccgacagatgctgtgacccgcaacgcgcgcgtg 296
DB ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 291 gtccatcgtgtcgcgtcgtctctgacatgatgctctccacgcgaacgatgcgcgtg 350
QY 297 cctggccaagggtttctacaactacggcccttcgtcgcgcgcgcacactcgttctcggg 356
DB || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 351 ccggccgacaaactctacactacacgcttcgtcgcgcgcgcgcgcgcctcccg 410
QY 357 cttcgcgacacaggttagcaccgactcaagaagcgcgaggtggccgcgtctcctccta 416
DB ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 411 cttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 470
QY 417 gacttccacagagacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 476
DB || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 471 gacttccacagacacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 530
QY 477 ctactgttcaacaggag--cgccgcgcacactccgactactgcacccgcgcgcgcgcgc 533
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 531 ctactgttcaagagagaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 590
QY 534 gtggccatgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 593
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 591 gtggcgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 650
XX
```



```
QY 355 ggcttcgacacaggttagacacccagctcaagaagcgag-----gtggccgctt 407
Db 386 ggcttcgacacaggttagacacccagctcaagaagcgagctggcgctggcgctt 445
QY 408 cctcgtcagaactccacagacagacagcggttgccgacgagcccgccgaccccta 457
Db 446 cctggcgagagctcgaacagacagcggttgccgacgagcccgccgacgagcccta 505
QY 468 ctcctgggctactgcttaacacagagcgcgccacct-----cagactactgca 521
Db 506 cgcttgggctactgcttaagagagagcggttgccgacgagcccgccgaccccta 565
QY 522 gcgagctcagtgcccatgtcgccgagcagaagtagtacttggcgcgcccgcccta 581
Db 566 gccagcgccagtgccgtgcgcggggaagaagtagtactacgcgcgcccgcccta 625
QY 582 gatctacacaaactaacactacgagcgccgagcgagccatcgccacgacgtgtcaa 641
Db 626 gatctacacaaactaacactacgagcgccgagcgagccatcgccgagccatcgc 685
QY 642 caaccggacgttggtcgctcgacgacgacgtgtgttttaagacggtgtgtgtctg 701
Db 686 caaccggacgttggtcgctcgacgacgacgtgtgttttaagacggtgtgtgtctg 745
QY 702 gatgagcgccgaatccaaactccttgagccacgagctgatacagcgccggtggagccc 761
Db 746 gatgagcgccgagtgcccaagcgtgtgtccacgagctacacggtgagtgagcgc 805
QY 762 ctggcgcgacagcagcgcggtggaggtgctgggtgagcaggtgtatatacacaatcat 821
Db 806 ctgcgggtgacagcgccgagcggtgaggtgaggtgaggtgaggtgaggtgaggtgag 865
QY 822 caacggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 881
Db 866 caacggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 925
QY 882 ctacaaagcgtactcgacactccttggtcgtacgtacgtgacacgtgactgctacaa 941
Db 926 ctacaaagcgtactcgacactccttggtcgtacgtacgtgacacgtgactgctacaa 985
QY 942 ccaaaagcgtctc 954
Db 986 ccaaaagcgtctc 998
```

RESULT 6

AAQ62518

ID AAQ62518 standard; cDNA; 1002 BP.

XX AAQ62518;

AC AAQ62518;

XX AAQ62518;

XX AAQ62518;

XX AAQ62518;

XX AAQ62518;

XX Antifungal; pathogen; resistance; transgenic organism; synergy;

KW crop protection; transgenic plant; chitinase; glucanase;

KW protein synthesis inhibitor; disease; ss.

XX

OS Hordeum vulgare L.

XX

FH Key Location/Qualifiers

FT CDS 64..864

FT FT /*tag= a

FT FT /product= Chitinase G.

FT FT sig_peptide 63..132

FT FT /*tag= b

FT FT mat_peptide 133..864

FT FT /*tag= c

FT FT polyA_signal 905..910

FT FT /*tag= d

FT FT /note= "Putative polyadenylation signal."

XX

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PN DE4234131-A.
XX 21-APR-1994.
XX 09-OCT-1992; 92DE-4234131.
XX 09-OCT-1992; 92DE-4234131.
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA Chet I, Ekes P, Gornhardt B, Jach G, Logemann J;
PI Mundy J, Schellj, Goernhardt B;
XX WPI; 1994-136599/17.
DR P-PSDB; AAR52577.
XX Transgenic organisms contg. at least 2 pathogen inhibiting genes
PT - esp. plants contg. genes with antifungal activity, show
PT synergistic increase in disease resistance, also new DNA transfer
PT vectors
XX Example 2; Page 13-14; 19pp; German.
XX This sequence encodes Chitinase G. Chitinase is an enzyme which
CC breaks down chitin, the major protein in insect exoskeletons. The
CC coding sequence may be used in the construction of transgenic
CC organisms, especially plants, to produce pathogen resistant
CC organisms. The genome of such transgenic organisms preferably
CC contains more than one gene with pathogen inhibiting activity/ each
CC gene under the control of active promoters. The two gene products
CC then show a synergistic increase in pathogen induced activity so that
CC the transgenic organisms have a greater degree of resistance or
CC resistance against a wider spectrum of diseases.
XX Sequence 1002 BP; 194 A; 329 C; 293 G; 186 T; 0 other;
SQ
```

Query Match 53.5%; Score 513.6; DB 15; Length 1002;

Best Local Similarity 81.1%; Pred. No. 4e-83;

Matches 597; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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QY 224 gggggggtctctctcattatctgcagctcgtcttctgacacagatgctgtgacacga 283
Db 128 ggggagctgtctcctcgtctgcgcacagtttgaccgcttctctcaccga 187
QY 284 acgacggtgctgctgccaaggggtctacacacgagcgtctgctgctgctgctgctg 343
Db 188 acgacggtgctgctgccaaggggtctacacacgagcgtctgctgctgctgctgctg 247
QY 344 actgcttctggtctgctgccaaggggtgacacaggtgacacagcgtgacacagcgtg 403
Db 248 cggcttctggtgctgctgccaaggggtgacacaggtgacacagcgtgacacagcgtg 307
QY 404 cgttctctgctgacattcctcagacagcagcgggtgctgctgctgctgctgctgctg 463
Db 308 ccttctctgacagacgtcctcagacagcagcgggtgctgctgctgctgctgctgctg 367
QY 464 cctactcctggtgctgctgctgccaaggggtgacacaggtgacacagcgtgacacag 523
Db 368 ccttctggtggtgctgctgctgccaaggggtgacacaggtgacacagcgtgacacag 427
QY 524 cgagctgcagtggtgctgctgccaaggggtgacacaggtgacacagcgtgacacagcgt 583
Db 428 cgagcgcacatggtgctgctgccaaggggtgacacaggtgacacagcgtgacacagcgt 487
QY 584 tctcacaactacaactacagcggcggtgacacaggtgacacagcgtgacacagcgtgac 643
Db 488 tctcacaactacaactacagcggcggtgacacaggtgacacagcgtgacacagcgtgac 547
QY 644 acccgacacttggtgctgacagcagcgtgctgctttaaagacggtgctggttctgga 703
Db 548 acccgacacttggtgctgacagcagcgtgctgctttaaagacggtgctggttctgga 607
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PD	23-JUL-1996.	
XX	04-AUG-1994;	94US-0286020.
XX	04-AUG-1994;	94US-0286020.
XX	(UNMS) UNIV MICHIGAN STATE.	
XX	Hajela RK, Sticklen MB;	
PI	WPI: 1996-353879/35.	
DR	P-PSDB; AAW00186.	
XX	Isolated chitinase gene derived from an American elm - used to	
PT	obtain prods. for inhibiting fungal infection of plants	
XX	Claim 1; Fig 1; 12pp; English.	
PS	This sequence represents the cDNA clone pHS2, which encodes a protein	
XX	having chitinase-activity derived from american elm. This protein	
CC	inhibits the fungus Ophiostoma ulmi, the causative agent of dutch	
CC	elm disease. The clone pHS2 may be used to transform E. coli cells	
CC	for the recombinant production of the chitinase-like protein. The	
CC	protein may be used in a composition to inhibit fungal infection of	
CC	elm trees.	
XX	Sequence 1225 BP; 322 A; 277 C; 313 G; 313 T; 0 other;	
SQ		

RESULT 12

QY	178	aatggtctgaagcggcgccaccccggtaaccggtaaccgcgccgcgcgctcc	237
Db	268	ggoggcagcgttagcat-----gacattggc	294
QY	238	tcaattatctcgaaagtctcttcgacagatgctgctgcacgcgaacacgocggtgc	297
Db	295	ggctcactatacaagctccgcctttaatgacatgctaagaacatgtaacgagtggtgt	354
QY	298	ctagccaagggtttctacaactaacgagcgccttgcgcgcgcgcgaactcgttctcgggc	357
Db	355	cctgcgaagggtttctacaactatgatgcttttatgtcgttcgaaggtttccctgcga	414
QY	358	ttgcgcaccacaggttagcacccagctcaaagaacgcgagagtgccgcggttctcgtctcaag	417
Db	415	tttgtctccaccggcgtatgataccacccgttaaaggagagattgctgttcttaggtcaa	474
QY	418	acttcccacagacacgcgcgggtgtgcgaacgcgcgcgcagcggccccctactccttgggc	477
Db	475	acttcccatgaacctacaggtgtggtgtgggaagtgacccgcagcgttcoatactcttgggga	534
QY	478	tactgttctcaaccagagcgcggcgccacctcgcactactgcacgcgcgactcgcgaagtgg	537
Db	535	tactgtcacaataggagcaaaccccttctcogattattgtttcttagtctactctgg	594
QY	538	ccatgtgcgcgggcaagaagtactcttcggcgcgcggcccatcagatctcacacaactac	597
Db	595	ccttgtgtcttcgggaagagatactttggccgtgtgtcccatctcaactctccttgggaactac	654
QY	598	aactacgggcgcggcgggcagggccatcggcacgcacactgtctcaacaacccggaccttgtg	657
Db	655	aactatggacagtgtggaaggccataggagcaaaaacctattaaacaacctgatctcgta	714

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:27:02 : Search time 142.45 Seconds
(without alignments)
1526.282 Million cell updates/sec

Title: US-09-534-229C-8

Perfect score: 960

Sequence: 1 atgagagagtggtggtggt.....accaaaggccgttcgatg 960

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2.6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgn2.6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2.6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2.6/prodata/2/ina/PCOTUS_COMB.seq:*
- 6: /cgn2.6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614.6	64.0	1151	1	US-07-704-288C-2
2	614.6	64.0	1151	1	US-08-093-372-1
3	614.6	64.0	1151	1	US-08-379-259-2
4	513.6	53.5	1002	1	US-08-457-797A-9
5	513.6	53.5	1002	1	US-08-812-025-9
6	513.6	53.5	1002	4	US-09-138-873A-9
7	358	37.3	1225	1	US-08-286-020-1
8	358	37.3	1225	1	US-08-603-919-1
9	349.2	36.4	943	2	US-08-475-427-15
10	349.2	36.4	943	2	US-07-842-165-15
11	347.6	36.2	1152	1	US-08-047-413-10
12	347.6	36.2	1152	3	US-08-229-050-10
13	347.6	36.2	1152	3	US-08-801-563-10
14	289.6	30.2	905	2	US-08-475-427-14
15	289.6	30.2	905	2	US-07-842-165-14
16	186.6	19.4	1317	3	US-07-791-931-1
17	178	18.5	1020	1	US-08-181-271A-7
18	178	18.5	1020	1	US-08-449-315-7
19	178	18.5	1020	1	US-08-444-803-7
20	178	18.5	1020	1	US-08-449-043-7
21	178	18.5	1020	1	US-08-456-265A-7
22	178	18.5	1020	1	US-08-455-416-7
23	178	18.5	1020	1	US-08-455-244-7
24	178	18.5	1020	1	US-08-454-876-7
25	178	18.5	1020	2	US-08-457-364-7
26	178	18.5	1020	2	US-08-456-262-7
27	178	18.5	1020	2	US-08-456-240-7

28	178	18.5	1020	2	US-08-455-736-7	Sequence 7, Appli
29	178	18.5	1020	2	US-08-971-217-7	Sequence 7, Appli
30	178	18.5	1020	4	US-09-350-600-7	Sequence 7, Appli
31	177.2	18.5	968	1	US-08-181-271A-12	Sequence 12, Appl
32	177.2	18.5	968	1	US-08-449-315-12	Sequence 12, Appl
33	177.2	18.5	968	1	US-08-444-803-12	Sequence 12, Appl
34	177.2	18.5	968	1	US-08-449-043-12	Sequence 12, Appl
35	177.2	18.5	968	1	US-08-456-265A-12	Sequence 12, Appl
36	177.2	18.5	968	1	US-08-455-416-12	Sequence 12, Appl
37	177.2	18.5	968	1	US-08-455-244-12	Sequence 12, Appl
38	177.2	18.5	968	1	US-08-454-876-12	Sequence 12, Appl
39	177.2	18.5	968	2	US-08-457-364-12	Sequence 12, Appl
40	177.2	18.5	968	2	US-08-456-262-12	Sequence 12, Appl
41	177.2	18.5	968	2	US-08-456-240-12	Sequence 12, Appl
42	177.2	18.5	968	2	US-08-455-736-12	Sequence 12, Appl
43	177.2	18.5	968	2	US-08-971-217-12	Sequence 12, Appl
44	177.2	18.5	968	4	US-09-350-600-12	Sequence 12, Appl
45	173.8	18.1	1153	2	US-08-475-427-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-07-704-288C-2
; Sequence 2, Application US/07704288C
; Patent No. 5399680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/07704,288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 64.0%; Score 614.6; DB 1; Length 1151;
Best Local Similarity 80.3%; Pred. No. 1.6e-112;
Matches 773; Conservative 0; Mismatches 179; Indels 11; Gaps 4;

Db 248 CCGCCCTCCGGGCTTCGGCACCACCGGACGCGCCGACGCCAGAGCGGAGGTGGCCG 307
QY 404 cgtctcctcagactccacagacacacgagcggtgagcgagcgagcgagcgagcgagc 463
Db 308 CCTCTCTAGCAGACACTCCACAGACACACCGCGGGTGGGATGTACCCGAGCGGG 367
QY 464 cctactctggggtactgttcaacacagagcgcgcgccactccgactactgcacgc 523
Db 368 CCTTCGGCTGGGCTACTGTTCAAGCAGGACGTGGCGCTCTCTCGACTACTGCACCC 427
QY 524 cgaactcgaagtggccatgtgcgcgggcaagaagtacttcggggcgggggcccatcaga 593
Db 428 CGAGCGCAACATGGCGCTGGCGCCCGGGAAGCGCTACTACGCGCGGGCCCAATCCAG 487
QY 584 tctcacacactcaactacgagcgcgcgagggcagccatcgacacgacgtctcaaca 643
Db 488 TCTCCACAACTACACTATGGACCTGCCGCGGGCCATCGGGGTGATCTCTGTGCCA 547
QY 644 accggacactgtgggtggagcgagcgagcggtgtcgtttaagacggggtgtgttctgga 703
Db 548 ACCCGGACCTGTGGTGGCAGGACGCCACTGTGGGCTTTAAGACGGGCATCTGTGTCTGA 607
QY 704 tcacgcgcaatcaccaagccttcagcaacacgtgatcagcgagcgagcgagcgagcct 763
Db 608 TGACGGCGGACCGCCCAAGCCATCGAGCATGTGTGATCGCGCGCCAGTGGAGCCGT 667
QY 764 cggcgccgacagggcggggaggggtgctgggtacggtgtgatcacaacacatcata 823
Db 668 CAGGGGTGACCGCGCGGACGAGCGGGTGGCGGTGTGTGATCACCACATCATCA 727
QY 824 acggtgggtcagtgagcgcgcgagcgagcgagcgagcgagcgagcgagcgagcgagc 883
Db 728 ACGGCGGGATCGAGTGGGTGATCGAGCGGACGAGCGCGGTGATCGAGTGGGTGTT 787
QY 884 acaagcgactcgactcctctggtgagcgagcgagcgagcgagcgagcgagcgagc 943
Db 788 ACAGCGCTACTGTGATCATCTCGGCGTGGCTACGGCAACAACTCGATTGTCTACAGC 847
QY 944 aaagcggttcgcata 959
Db 848 AGAGACCTTCGGCTA 863

RESULT 7

US-08-286-020-1
; Sequence 1, Application US/08286020
; Patent No. 5539095
; GENERAL INFORMATION:
; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
; TITLE OF INVENTION: A Chitinase cDNA Clone From a
; TITLE OF INVENTION: Disease Resistant American
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS 5.00
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,020
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No. 5539095e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1225
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; HYPOTHEetical: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Ulmus Americana
; STRAIN: NPS 3-487
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: chitinase encoding DNA
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA needed for chitinase
; OTHER INFORMATION: in elm.
; PUBLICATION INFORMATION:
; US-08-286-020-1

Query Match 37.3%; Score 358; DB 1; Length 1225;

Best Local Similarity 64.0%; Pred. No. 3e-62;

Matches 575; Conservative 0; Mismatches 290; Indels 33; Gaps 1;

QY 58 gccagagcaatcgcggtctgcagcgcgagcgagcgagcgagcgagcgagcgagcgagc 117
Db 148 GCAGAGCAATGTGAGCAAGCCAAAGTGGGGTGCAGTGTGTCCCGTTGGGCTCTGTGTCAGC 207
QY 118 agdtgggttttcgagcaccactccgactcagcgagcgagcgagcgagcgagcgagc 177
Db 208 AAATTGGGTGGTGGGAGCACAACAGTACTGTGTGATGCTGCCAAGCAATGT 267
QY 178 aatgggtcagcgcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 237
Db 268 GCGGCGAGCGTAGCGAT-----GACATTGGC 294
QY 238 tccattatctcagctcgtctcttcgacagatgctgacgagcgagcgagcgagcgagc 297
Db 295 GGTCTCATATCAAGCTCCGCCCTTTAATGACATGCTTAAGCATCGTAACGACGCGTGTGT 354
QY 298 ctggcgaaggggtttcacaactcagcgagcgagcgagcgagcgagcgagcgagc 357
Db 355 CCGTCCCAAGGGGTTTTACACCTATGATGCTTTTATTCGGCTGCCAAGGCTTTCCTGCA 414
QY 358 ttgcgaccacaggttagcaccgacgagcgagcgagcgagcgagcgagcgagcgagc 417
Db 415 TTGGGCTCCACCGCGGATGATACACCCGTAAAGGAGATGCTGCTTTCTTAGGTCAA 474
QY 418 acttccacgagacgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 477
Db 475 ACTTCCCATGAACTACAGGTGGGTGGGCAAGTGCACCCGACGCGTCCATCTCTTGGGA 534
QY 478 tactgttcaaccagagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 537

Db 535 TACTGCTACATAGGAGCAAAACCTTCTCCGATTATTGTTCTTTAGTCTACTTGG 594
QY 538 coattgcccgcgcaagaagtacttcggcgccggcccaatccagatctcaacaactac 597
Db 595 CTTGTGCTTCCGAAAGAGATACATTGGCCGTGGTCCCAATCAACTCTCTCGGAACATC 654
QY 598 aactacggccgcggcgccagccatcgccacgcacccctgctcaacaacccggaccttg 657
Db 655 AACTATGACAGTGTGAAGGCCATAGAGCAACACCTATTAAACACCTGATCTCGTA 714
QY 658 gogtgcgacgcacgcgtgctgttaagacgcggtgtgtgttctgagtcgacgcgcaatca 717
Db 715 GCAACTGACCCCTGTCATTCTCTCAAAAGCGCTTATGTTCTGGATGACCCACAGTCA 774
QY 718 ccaagccttcgacgcacgcgtgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 777
Db 775 CCNAGCCCTCGGCATGACGTATCACCGGAAGTGGAGTCTTCCGGCACCCAGCAG 834
QY 778 gcggcggggaggtgctgggtgacgtgtgacgtgtgacgtgtgacgtgtgacgtgtgac 837
Db 835 TCGGCCGCGGAGTTCGGGCTACGGCGTATCACCAACATTATCAACCGTGGATAGAA 894
QY 838 tcggcgccgcgacgc 897
Db 895 TCGGGGAAAGGTCAGTCTCTCAGTGGTGGATCGGATTGGATTCTACAGAGGTACTGT 954
QY 898 gacctctctggcgtcagctacgtgtgacacccctggacgtgtgacacccaaaggcgttcg 955
Db 955 GATATCCTTAGAGTTGGCTATGGGAACAATCTTGATGCTATACCAAGAGGCTTTTG 1012

RESULT 8

US-08-603-919-1
; Sequence 1, Application US/08603919
; Patent No. 5728382
; GENERAL INFORMATION:
; APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
; TITLE OF INVENTION: A Chitinase cDNA Clone From a
; TITLE OF INVENTION: Disease Resistant American
; TITLE OF INVENTION: Elm Tree
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS 5.00
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,919
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MSU 4.1-207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEX: No 5728382e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1225
; TYPE: Nucleic Acid
; STRANDEDNESS: Single

; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Ulmus Americana
; STRAIN: NPS 3-487
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: N/A
; HAPLOTYPE: N/A
; TISSUE TYPE: N/A
; CELL TYPE: N/A
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE: N/A
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: chitinase encoding DNA
; LOCATION:
; IDENTIFICATION METHOD: sequencing
; OTHER INFORMATION: DNA needed for chitinase
; OTHER INFORMATION: in elm.
; PUBLICATION INFORMATION:
US-08-603-919-1

Query Match 37.3%; Score 358; DB 1; Length 1225;
Best Local Similarity 64.0%; Pred. No. 3e-62;
Matches 575; Conservative 0; Mismatches 290; Indels 33; Gaps 1;

QY 58 gccgagcaatgcgctgcgagccgcccgcgagtcgcccacactgcctctgtcgcagc 117
Db 148 GCAGAGCAATGTGAAGCCCAAGCTGGGGGTGCAGTGTGCCGTGGGGGTCTGCTGCAGC 207
QY 118 aagttcggttctgcgcacccctccgactactgcgcgcgcgcgcgcgcgcgcgcgcgcgc 177
Db 208 AAATTTGGTGTGGGACCAACAGAGTACTGTGTGATGGCTGCCAAAGCCCAATGT 267
QY 178 aatgctgcgagccgcccgc 237
Db 268 GCGGCGAGCGGTAGCGAT-----GACATTGGC 294
QY 238 tccattatctgcagtcgctcttcgacacagatgcgtgcacgcgcgcgcgcgcgcgcgcgc 297
Db 295 GGTCTCATATCAAGCTCCGCTTTAATGACATGCTTAAGCATCGTAACGACGGTGGTTGT 354
QY 298 ctggccaaagggttctcaactacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 357
Db 355 CTTGCCAAGGGGTTTACACCHATGATGCTTTATGCGGCTGCCAAGGCTTCCCTGCA 414
QY 358 ttccgacacacaggttagcaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 417
Db 415 TTTGGCTCCACCGCGGATGATACACCCCTAAAGGAGATTGCTGCTTTAGTCA 474
QY 418 acttcccacgagacgc 477
Db 475 ACTTCCCATGAAACTACAGGTGGTGGCAAGTGCAACCGGCTCCATACCTTTGGGGA 534
QY 478 tactgttcaaccagagcgccgc 537
Db 535 TACTGCTACATAGGAGCAAAACCTTCTTCCGATTATTGTTCTTTAGTCTACTTGG 594
QY 538 coattgcccgcgcaagaagtacttcggcgccggcccaatccagatctcaacaactac 597
Db 595 CTTGTGCTTCCGAAAGAGATACATTGGCCGTGGTCCCAATCAACTCTCTCGGAACATC 654
QY 598 aactacggccgcggcgccagccatcgccacgcacccctgctcaacaacccggaccttg 657
Db 655 AACTATGACAGTGTGAAGGCCATAGAGCAACACCTATTAAACACCTGATCTCGTA 714
QY 658 gogtgcgacgcacgcgtgctgttaagacgcggtgtgtgttctgagtcgacgcgcaatca 717

Db 715 GCAACTGACCCCTGTGATCTTCCATCAAAACGGCCCTTATGTTCTGGATGACCCCAAGTCA 774
QY 718 ccaagccttcagcacacgtatgatacagggcggtgagccctcgggcgccgacag 777
Db 775 CCAAAACCCCTCGTCCATGACGTCATACCGGAAGATGAGTCTCTCCGSCACCGACGAG 834
QY 778 gggcggggaggggtgctgggtacgtgtgatacacaacatacatcaacaggtgggtcgag 837
Db 835 TCGGGCGGGCGGAGTTGCGGGCTACGGCGTGTATCAACCAATTATCAACGGTGGGATAGAA 894
QY 838 tggcgggcgggcgaggaacggcggtgctgcgcacgggatcggggtctacaagcgctactgc 897
Db 895 TCGGGGAAGAGTCAGGTTCTCAGGTGGTGGATCGGATTCGATTCACAGAGGTACTGT 954
QY 898 gacctctggggtcagctacgtgatacaccctgggactgtatacaacaaaggcgcttcg 955
Db 955 GATATCCTTAGAGTTGGCTATGGGAACAATCTTGATTGCTATAAACAGAGCGCCTTTTG 1012

RESULT 9
US-08-475-427-15
; Sequence 15, Application US/08475427
; Patent No. 5859340
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: PIGNARD, Annie
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,427
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,165
; FILING DATE: 01-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00607
; FILING DATE: 21-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90 09460
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/564/BEDL
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-475-427-15

Query Match 36.4%; Score 349.2; DB 2; Length 943;
Best Local Similarity 63.3%; Pred. No. 1.6e-60;
Matches 581; Conservative 0; Mismatches 313; Indels 24; Gaps 2;
QY 45 cgtgtctgcgacgcgagcaatgcggtcgcagcgcgcgggcgagcgtgcccacaactg 104
Db 12 CCTCTCTGCTCGGAGACAAATGTTGGTGTGTAAACACCAATGACTATTGTGGCCCTGGCAA 71
QY 105 cctctctgcagcaagtctcggtttctgcgcgaccactccgactactgcggccaccggc-- 162
Db 72 TCCTCTGCTGAGCAAAATTTGGTGGTGTGTAAACACCAATGACTATTGTGGCCCTGGCAA 131
QY 163 -tcacagaccagtcgaatgctgcgcgagcgcgcccccgggtaccggtaacggacccctc 221
Db 132 TTGCCAGAGCGACGTGCGCTGGTGTGCTCCCA-----CACCACCCGG 170
QY 222 cggcgcggtctctctccattatctgcagtcgctcttcgaccagatgctgtgcacg 281
Db 171 TGGTGGGATCTCGGCAGTATCACTCAAGTTCATGTTTGATCAGATGCTTAAGCATCG 230
QY 282 caacgacgcggcgtgctgcccgaagggtttctacaactcggcgcccttgcgcccgcc 341
Db 231 CAACGATATGATGATGCCAAGGAAGGATTTCTACAGTTACATGCTTTTATCAATGCTGC 290
QY 342 caactcgtctcgggttcgcgcacacaggttagcacgcagtcgaagaagcgaggtggc 401
Db 291 TAGGTCTTTTCTCGCTTTGGTGTACTAGTGTGATACACTGCCCGGTAAAGAGAAATCGC 350
QY 402 cgcgtctctcgcagactccacagagacgcgcgcgggtgcccgcgcgcgcgcgcgcgcgc 461
Db 351 GGTCTTCTCGCCCAACCTCCCATGAACTACAGGAGGATGGGACACACACAGATGG 410
QY 462 cccctactcctgggttactgtcttaaccaggagcgcgccacctcccgactactgcac 521
Db 411 TCCATACGCGTGGGGTTACTGCTGGCTTAGAGAACAAAGTAGCCCGCGCACTACTGTAC 470
QY 522 gcgagctcgcagtgccatgtgcgcgcggcgagccatcgccatcgccacgcacctgtcaa 581
Db 471 ACCAAGTGTGTCAGTGGCCTTGTCTCTGTGCGAAATATTTCCGAGGAGGCCCATCCA 530
QY 582 gatctcacacaactacaactacgcgcgcgggcgagccatcgccacgcacctgtcaa 641
Db 531 AATTTCACACACTACAACTACGGACCTTCTGGAAGAGCCATAGGAGTGGACCTCTCTAAA 590
QY 642 caacccggacctgtggcgtcgc 701
Db 591 CAATCTCTGATTTAGTGGCCACAGATCCAGTAATCTCAAGTCACTCTCTCTGTTTG 650
QY 702 gatgacgcgcgaatcacccaagccttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 761
Db 651 GATGACFCCICATFACCAAAACCTTCTTCCAGATGTATCATTTGGAGATGGCAACC 710
QY 762 ctggcgcgccgacacgagcgcggggggaggtgcttgggtaacggtgtgatcaccaacatcat 821
Db 711 ATCGTCTGCTGACCGCGCAGCCAAATCGTCTCCCTGGATTTGGTGTATCATCAGAACATCAT 770
QY 822 caacggtgggtcgcagtcgcggcgcgggcgaggaacggcggtgctgcgcgcgcgcgcgcgcgc 881
Db 771 CAATGGTGGCTTGAATGTGTGTGCTGTCACCTGACTCAAGGGTCCAGGATCGCATTTGGTT 830
QY 882 ctacaagcgtactgcgacctcttggcgtcagctacggtgacaacctgactgtctaca 941
Db 831 TTACAGGAGGTATTCAGTATTTCTTGGTGTAGTCTTGGTGTGACAAATCTTGATTCGGGAAA 890
QY 942 ccaaaaggccgttcgcata 959
Db 891 CCAGAGGCTCTTTGGAAA 908

RESULT 10
US-07-842-165-15
; Sequence 15, Application US/07842165
; Patent No. 5932598

GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: EIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842.165
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-842-165-15

Query Match 36.4%; Score 349.2; DB 2; Length 943;
Best Local Similarity 63.3%; Pred. No. 1.6e-60;
Matches 581; Conservative 0; Mismatches 313; Indels 24; Gaps 2:

QY 45 cgtgtctgcagccgacgcaatcggtttctgcggcaccacctccgactactcggcaccgcgc-- 162
DB 12 CTTCTCTGCCCTGGGAGACATGTTGGTTCGAGCGGGAGGTGCGGTTGTGCTCGGG 71
QY 105 cctctgtcagcaggaattcgtttctgcggcaccacctccgactactcggcaccgcgc-- 162
DB 72 TCTCTGCTGCAGCAAAATTTGGTGTGGTAAACCAATGACTATTGTGGCCCTGGCAA 131
QY 163 tgcagagcagtgcaatggtcgtcagcggcgccaccgcggtaccggtaccgaccctc 221
DB 132 TTGCCAGAGCCAGTGCCTCGTGGTCCCA-----CACCACCCGG 170
QY 222 cggcgccggcgtcctctccattatcgcagtcgctctcaccagatcgtctcacgc 281
DB 171 TGGTGGGATCTCGGCAGTATCATCTCAAGTTCCATGTTGATCAGATGCTTAAGCATCG 230
QY 282 caacgacgcggtcgtcgtcggcgaaggggtctacacactacgcgcttcgtcgcgcgcgc 341
DB 231 CAACGATATGATGCCAAGGAAGGATCTTACAGTTACATGCTTATCAATGCTGTC 290
QY 342 caactcgttctcgttctcgttcgacacacaggttagcaccgacgtcaagaagcgcggtg 401
DB 291 TAGGTCCTTTCTCGCTTGGTGTACTAGTGGTATACCACTGCCCGCTAAAGAGAAATCGC 350
QY 402 cgcgttctcgtcgtcgtcgttccaccagacgacgacggttggtccgacggtccgcgacg 461

DB 351 GGCTTTCTTGGCCCAACCTCCCATGAAACTACAGSAGATGGCAACAGCACCAGATGG 410
QY 462 cccctactcctgggctactgcttcaaccagagcgcgcgccacctccgactactgtaac 521
DB 411 TCCATACCGTGGGTTACTGCTGGCTTAGAGAAACAAGTAGCCCCGGGACTACTGTAC 470
QY 522 gcgagctcgcagtgccatgtgcgcgggcaagaagtacttcggcgcgccgcccacatca 581
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DB 531 AATTTACACAACTACAACTAGGACCTTGTGGAAGAGCCATAGGAGTGGAGCTCCTAAA 590
QY 642 caaccggacccttggtggtcggacgacgacggtgcttttaagacggtgtgtgtctg 701
DB 591 CAATCCTGATTAGTGGCCACAGATCCAGTAAATCATTTCAAGTCAAGTCAAGTCAAGTCA 650
QY 702 gatgacgcgcaatcaccccaagccttcgagccacgacgtatcagcgccggtggagccc 761
DB 651 GATGACTCTCAATCACCACCAACCTTCTTGCACGATGTATCATTTGGAAGATGGCAACC 710
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RESULT 11
US-08-047-413-10
; Sequence 10, Application US/08047413
; Patent No. 5670706
; GENERAL INFORMATION:
; APPLICANT: Cornelissen, Bernardus J.C.
; APPLICANT: Melchers, Leo S.
; APPLICANT: Meulenhoff, Elisabeth J.S.
; APPLICANT: van Roekel, Jeroen S.C.
; APPLICANT: Seia-Buuriage, Marianne B.
; APPLICANT: Vloemans, Alexandra A.
; APPLICANT: Woloshuk, Charles P.
; APPLICANT: Bol, John F.
; APPLICANT: Linthorst, Hubertus J.M.
; TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
; TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/047,413
; FILING DATE: 19-APR-1993


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Db 183 TTCCAGAGCCAGTGCCTCGGTGCCA-----CACCACCGG 221
QY 222 cggcgccgctctctccattatctcgcagctcttcgaccagatctgctgcacg 281
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Db 522 ACCAAGTGTGAGTGGCTTGTCTCTGCTCGGAAATATTTCGGACGAGGCCCATCCA 581
QY 582 gatctcacaaactacaaactaagggcgcgcgggcgagggcgacacgacactgctcaa 641
Db 582 AATTTTCACACAACTACAGCTACGAGACCTTGTGAAGAGCCATAGGAGTGGACCTCTAA 641
QY 642 caaccgagacttgctgctgagcgcgacgctgtgtttaaagcggctgtgtgtctg 701
Db 642 CATCTGATTTAGTGGCCACAGATCCAGTAATCTCATCAATCAGCTCCTCTGGTTTG 701
QY 702 gatgacgcgcgaatcccaagccttcagccacgacgctgatcacggcggtggagcc 761
Db 702 GATGACTCTCAATACCAAAACCTTCTGCCACGATGTATCATATGGAAGATGGCAACC 761
QY 762 ctggcgccgacacagcgcgcgggggggtgctggtgagtggtgagtgatccacacatcat 821
Db 762 ATGCTGTGCTGCGCGCGACCAATCTCTCCCTGATTTGGTGTATCATCAGCAATCAT 821
QY 822 caacggtggctgagtgcgcgcgcgagcgcgctgctgcgcgacgagcggtt 881
Db 822 CAATGFGCTTGGATGTGGTGTGGCAGTACTCAAGGTCAGGATCGCATGGGTT 881
QY 882 ctacaagcgtactgcactccttgctgctgacgtaagtgacagtgacaaactgactgtaca 941
Db 882 TTACAGGAGGATTTGAGTATTTCTGTGTGTAGTCTCTGTGTGACAACTTTGATTCGGAAA 941
QY 942 ccaagcgcttcgcata 959
Db 942 CCAGAGGCTTTTGGAAA 959

RESULT 14
US-08-475-427-14
; Sequence 14, Application US/08475427
; Patent No. 5859340
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Michel
; APPLICANT: GRISON, Rene
; APPLICANT: LEGUAY, Jean-Jacques
; APPLICANT: PIGNARD, Annie
; APPLICANT: TOPPAN, Alain
; TITLE OF INVENTION: Recombinant gene coding for a protein
; TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
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; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,427
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,165
; FILING DATE: 01-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00607
; FILING DATE: 21-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90 09460
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/564/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-475-427-14

Query Match 30.2%; Score 289.6; DB 2; Length 905;
Best Local Similarity 60.6%; Pred. No. 7.4e-49;
Matches 516; Conservative 0; Mismatches 324; Indels 12; Gaps 2;

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QY 467 actcctgggctactgcttcaaccagagcgcgccacactcgcactactgcagcgaga 526
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2002, 16:24:10 ; Search time 3076.35 Seconds
(without alignments)
3353.307 Million cell updates/sec

Title: US-09-534-229c-8

Perfect score: 960

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Gapop 10.0 , Gapext 1.0

Searched: 11951937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: em_estin:*
4: em_estom:*
5: em_estpl:*
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8: em_estov:*
9: em_hic:*
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11: gb_est2:*
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13: gb_gss:*
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19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_othe:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	578.4	60.2	705	11	BG367460
2	572.8	59.7	711	11	BG367616
3	568	59.2	681	10	BE705117
4	515.8	53.7	805	11	BG365536
5	486	50.6	935	11	BG365857
6	459.4	47.9	816	11	BF064981
7	458.2	47.7	729	10	BE602672
8	453.6	47.2	937	11	BG365887
9	439	45.7	742	11	BG365634
10	436.8	45.5	682	11	BG416746
11	433.2	45.1	623	11	BG368852
12	430	44.8	806	11	BG414551

13	423.4	44.1	908	11	BG415203
14	420.6	43.8	625	11	BG368854
15	416.2	43.4	969	10	BE454366
16	415	43.2	465	10	BG500345
17	399.4	41.6	711	11	BG366386
18	394	41.0	711	10	BE455238
19	392	40.8	652	10	AL499683
20	391.8	40.8	502	10	BE500112
21	389.6	40.6	653	11	BG313150
22	389	40.5	899	10	BE603335
23	388.4	40.5	692	11	BG369588
24	385.6	40.2	943	11	BG365157
25	385	40.1	753	11	BG365326
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27	384	40.0	632	10	BE598085
28	379.6	39.5	731	11	BG363340
29	375.6	39.1	710	11	BG366294
30	373.6	38.9	731	10	BE602548
31	365.4	38.1	693	10	AL500402
32	358.8	37.4	956	10	BE454432
33	356.6	37.1	732	11	BG836200
34	356.4	37.1	764	11	BG836379
35	355	37.0	600	10	BE597800
36	353	36.8	704	11	BG836345
37	351.4	36.6	572	10	AW585282
38	350.2	36.5	731	11	BG836493
39	349.6	36.4	860	11	BG365415
40	347.2	36.2	628	10	BE195290
41	345.6	36.0	616	10	BE405578
42	345.6	36.0	652	10	BE602137
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ALIGNMENTS

RESULT 1

LOCUS BG367460 705 bp mRNA EST 08-MAR-2001
DEFINITION HVSMEI0012F13f Hordeum vulgare 20 DAP spike EST library HVCNDA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMEI0012F13f, mRNA sequence.

ACCESSION BG367460

VERSION BG367460.1

KEYWORDS GI:13256559

SOURCE EST.

ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 705)

AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu

,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo

,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and

Wood,T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

Contact: Wing RA

Clemson University

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTACCTCTACTAAAGG

High quality sequence stop: 690.

Location/Qualifiers

1..705

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

FEATURES

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/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 117 a 261 c 219 g 108 t
ORIGIN

Query Match 60.2%; Score 578.4; DB 11; Length 705;
Best Local Similarity 94.7%; Pred. No. 1.1e-98;
Matches 610; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
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QY 121 ttccgtttctgcggcaaccactccgactactcgtggcaccggctgcccagagccagtgaat 180
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LOCUS HVSMEI0012P08f Hordeum vulgare 20 DAP spike EST library HVCDA0010
DEFINITION (20 DAP) Hordeum vulgare cDNA clone HVSMEI0012P08f, mRNA sequence.
ACCESSION BG367616
VERSION BG367616.1 GI:13256715
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 711)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D., and
Wood, T.
Development of a genetically and physically anchored EST resource
for barley genomics
Unpublished (2000)
Contact: Wing, R.
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTACCTCTACTAAAGG
High quality sequence stop: 678.
Location/Qualifiers
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/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEI0012P08f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HVCDA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 118 a 260 c 224 g 109 t
ORIGIN

Query Match 59.7%; Score 572.8; DB 11; Length 711;
Best Local Similarity 94.5%; Pred. No. 1.2e-97;
Matches 616; Conservative 0; Mismatches 32; Indels 4; Gaps 2;
QY 1 atagaggaattgtgtgtggtgcatgctgcccggcgcttcctccgtgtgtcgcaagcc 60
Db 60 ATGAGAGGACTTGTGTGTGGGCAATGCTGCCGCGGCTTCGCCGATCTGTACAGCC 119
QY 61 gagcaatgcggtcgcgagcgccggcgagcgtgcccccaactgcctctcgtcagcaag 120
Db 120 GAGCAGTGGGCTTCGACAGCGCGGGGACGTGCCCAACTGCCTCTGCTGCAGCAG 179
QY 121 ttccgtttctgcggcaaccactccgactactcgtggcaccggctgcccagagccagtgaat 180
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QY 298 ctggcaagggtttctacaactacggccttcgtgcccgcgcgcgaactcgtttctgggc 357
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QY 358 ttccgaccacaggtagcaccgagctcaagaagcgaggtgcccgttcctcgtcag 417
Db 420 TTCGACACACGGGTGCGGCTCCGACGTGAGGAGCGGAGGTGGCGGCTTCCTCGCACAG 479
QY 418 acttccacagagacgacggcggtgtgcccagcgccgacggccctactcctggg- 476
Db 480 ACCTTCCACAGACACCGCGGGGTGCGGACGCGGCGCCGCGGCGCCCTACTCTCGGGC 539


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RESULT 7
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LOCUS HVSMEH0101A21f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0101A21f,
mRNA sequence.
ACCESSION BE602672
VERSION BE602672.1 GI:9860233
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 729)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 713.
FEATURES
source
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/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0101A21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/TO
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 120 a 259 c 239 g 110 t 1 others
ORIGIN
Query Match 47.7%; Score 458.2; DB 10; Length 729;
Best Local Similarity 80.9%; Pred. No. 3.1e-76;
Matches 546; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 224 gggcggggtctctccattatctcgcagtcgtcttcttgcacagatgctgtgcacgcga 283
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 56 GCGGAGCGGTGCTCTCCATCATCTCGCGGCACAGTTCGACCGCATGTGCTGCACCGCA 115
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 284 acgacgcggtgcgtggccaagggttctacaactagcgcccttcgacgcgcga 343
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 AGACGGCGCCTGCCAGGCGCAGGGCTTCTACACCTACACCGCTTCGTCGCGCGCAT 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 344 actcgtctcgggtctcgacacacaggttagcaccgacgtcgaagcgcgaggtgcccq 403
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 CTGCTCTCCGGGCTCGCAGCAGCGGACCGCCGACGCCGACAGAGCGGAGGTGGCG 235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 404 cgtctcgtcagactccacagacacgcggcggttgccgacggcgccgcagcgcc 463
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 CCTTCTGCGCCAGACCTCCACGAGACACCGCGGATGGGCGACGCGACCGCGGG 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 464 cctaactctggggtactcgttcaacaggagcgcgccacctcgcactactgcaagc 523
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Db 547 ACCGGGACCTGGTGGCCACGACGCCACTGTGGCGTTTAAAGACGCCCATCTGGTCTTGA 606
Qy 704 tgacgcgcgaatcaccaagccttcgcagccacgacgtgacacgagcggcggtggagccct 763
Db 607 TGACGGGCGACACGCCCAAGCGTGCAGCCATGTGTGATCGCGGCCCATGGACCCCGT 666
Qy 764 cggcgccgacacgagcgcgcggtgctgctggtgacggtgacggtgacacacatcatca 823
Db 667 CAGGGGCTTACAGCGCGCGCAAGCGGCTGCCCGGTTTGGGGTGATCCCCAAATCATCA 726
Qy 824 acgtgggctcgagtcgagcgcgcgcgagcg 853
Db 727 ATGGGTGAACACAGTGGGTCACTGTCAAG 756

RESULT 13
BG415203 908 bp mRNA EST 13-MAR-2001
LOCUS HVSMEK0005116f Hordeum vulgare testa/pericarp EST library
DEFINITION HVSMEK0005116f (normal) Hordeum vulgare cDNA clone HVSMEK0005116f, mRNA
sequence.
ACCESSION BG415203
VERSION BG415203
KEYWORDS EST.
SOURCE BG415203.1 GI:13320754
organism Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 908)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 815.
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/tissue_type="testa/pericarp"
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/notes="Vector: lambda2AP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ to
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 202 a 257 c 266 g 181 t 2 others
ORIGIN

Query Match 44.1%; Score 423.4; DB 11; Length 908;
Best Local Similarity 82.7%; Pred. No. le-69;
Matches 484; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 375 caccgagtcgaagcgcgaggtggcggttctcgtcagacttcccccagagacac 434
Db 1 CGCCGACGCCAGAGCGCGAGGTGGCGGCTTCTGTGCCCAAACTCCACGAGACCAC 60
Qy 435 cggcggtggcgagcgcgcccgagggccctactctctggtggttactgttcaaccagg 494

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Db 61 CGGGGATGGCGGACGGCAGCCGAGCGGGGCTTCGGCTTGGGGCTACTGCTTCAAGCAGA 120
Qy 495 gcgcggcgcacccctccgactactcaagcgcagctcgagtgagcgcagtgagcgcagcaa 554
Db 121 ACGGCGGCGCCCTCCCGACTACTGCACCCCGAGGCGACAGTGGCGGTGGCGCCCGGGAA 180
Qy 555 gaagtactctggcgcgcgcccatccagatctcacacaactacacactacgagcgcgcg 614
Db 181 CGCTACTACGGCGCGGGCCCATCCAGCTCTCCCAACACTACACTATGACCTGCGCGG 240
Qy 615 gcaggccatcgccaccgacctgtctcaacaccccgagacctgtgctgctgagcgagacct 674
Db 241 CCGGCGCATCGGGTTCGATCTGTGTCGACCCGAGACCTGTGTGGCCACGACGACCACTGT 300
Qy 675 gtcgttaagacgcggtgtgtgtctggtatcacccgcaatcaccccaagccttcagacca 734
Db 301 GCGGTTTAAAGACGGCCAFCTGTGTGTGATGACGGCGAGCGCCCAAGCGCTCGAGCCA 360
Qy 735 cgagctgatacgcggcggtgagccctcgccgcgaccagcgcgcggtgaggtggtgcc 794
Db 361 TGCTGTGATCGCGGCCAGTGGAGCCCGTCAAGGGGCTGACCGGGCGCGAGGCGGTGCC 420
Qy 795 tgggtacggtgtgatcaccacacatacatcaacggtggtggtgagtcgagtcgagtcgag 854
Db 421 CGGGTTTGTGTGATACCAACATCATCAATGTTGGGTGGGATCGTGTGTCACGACAGGA 480
Qy 855 cgccgctgtcccgacgagatcggtttctacaagcgtactcgacacctccttgcgtcag 914
Db 481 CAGCGGTGTCGCCCATCGAATCGGGTTTACAGCGCTACGTGTGACATCTCCGCGTGG 540
Qy 915 ctacggtgacacctggactgtctacacacacacacacacacacacacacacacacacac 959
Db 541 CTACGGCAACAACCTCGACTGCTACACACGAGACACCTTCGCTTA 585

RESULT 14
BG368854 625 bp mRNA EST 08-MAR-2001
LOCUS HVSMEI0020P07f Hordeum vulgare 20 DAP spike EST library HVSMEI0020P07f, mRNA sequence.
DEFINITION (20 DAP) Hordeum vulgare cDNA clone HVSMEI0020P07f, mRNA sequence.
ACCESSION BG368854
VERSION BG368854.1 GI:13257955
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 625)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 606.
Location/Qualifiers
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/organism="Hordeum vulgare"
/cultivar="Morex"
/db.xref="taxon:4513"
/clone="HVSMEI0020P07f"

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 1. Triticeae; Hordeum.
 (bases 1 to 969)

Wing, R., Closer, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu,
 Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo,
 T., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
 Wood, T.

development of a genetically and physically anchored EST resource
 for barley genomics

Unpublished (2000)

On Jul 26, 2000 this sequence version replaced gi:94562873.

```

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Tel: 864 656 7288
Fax: 864 656 4293
Email: wing@clemson.edu
Seq primer: AATTACCCCTCACTAAGGG
High quality sequence stop: 616.
Location/Qualifiers
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/cultivar="Morex"
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/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/To
order a clone see http://www.genome.clemson.edu/orders"
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BASE COUNT
ORIGIN

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[illegible]

Tue May 7 10:52:46 2002

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Db 608 GGTTCGTGATGACGGCGCANCGCCCAAGCCGTGAGCATGCTGTGATCGCCCGCCOAG 667
Qy 754 tggagccctcgggcccagaccagcgcggggaggggtgcctgggtacgggtgtgatacc 813
Db 668 TGGAGCCCGTTAAGGGCTGACCGGGCCGCAAGGGGGTGCCCGGTTGGTGTGATCACC 727
Qy 814 aacatcatcaacggtgggctcagtgcgggcgcgaggacggccggtgtcgcgcagccgg 873
Db 728 CACATCATTAATGGGGGATTCAATGTGTACCGGACCGAGAAACCGTTTCGNCCAICCA 787
Qy 874 atcgggttctacaagcgtactgacacctcttgg 908
Db 788 AATGGGTTTACAGCGCCTCTGGGACTTCCTCGG 822

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